STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To:

Wednesday, May 08, 2002 11:04 AM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/802520

Subject:

Please rush. Thanks Chris

-----Original Message-----Fr m:

Davis, Minh-Tam

Sent:

Wednesday, May 08, 2002 10:53 AM

To:

Chan, Christina

Subject:

Rush search request for 09/802520

Please in commercial data base and in issued patent files 1) SEQ ID NO:1 and 2.

Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

FOR OFFICIAL USE ONLY

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Location:
Date Picked Up: 5/8/102
Date Completed: 5/4/60
Searcher Prep/Review:
Clerical:
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Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appl:	Sequence 3, Appl:	Sequence 46, Appl	Sequence 46, Appl	Sequence 46, App.	Sequence 46, Appl	Sequence 9, Appl:	Sequence 1, Appl:	Sequence 8, Appl:	Sequence 7, Appl:	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 2, Appli

ALIGNMENTS

Oy 306 GLLSFFFANVHVAYSLCLDMRRSI	Query Match 35.6%; Best Local Similarity 100.0%; Matches 173; Conservative Qy 246 DFYKIPIBIVNKTLPIVAITLLS; Db 1 DFYKIPIBIVNKTLPIVAITLLS;	Sequence 8, Application US/09323873A Patent No. 6329503 GENERAL INFORMATION: APPLICANT: Daniel E. Afar APPLICANT: Consiel E. Afar APPLICANT: Rene S. Hubert APPLICANT: Kahan Leong APPLICANT: Arthur B. Raitano APPLICANT: Steve Chappell Mitchell TITLE OF INVENTION: NOVEL SERPENTINE TRANS TITLE OF INVENTION: NOVEL SERPENTINE TRANS TITLE OF INVENTION: MOWER: US/09/323,873A CURRENT APPLICATION NUMBER: US/09/323,873A CURRENT FILING DATE: 1999-06-01 PRIOR APPLICATION NUMBER: 60/087,520 PRIOR FILING DATE: 1998-06-01 PRIOR APPLICATION NUMBER: 60/091,183 PRIOR FILING DATE: 1998-06-30 NUMBER OF SEQ ID NOS: 32 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 173 TYPE: PRT ORGANISM: Homo Sapiens US-09-323-873A-8
GLLSFFFAMYHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGI 365	atch 35.6%; Score 901; DB 4; Length 173; al Similarity 100.0%; Pred. No. 1.8e-85; 173; Conservative 0; Mismatches 0; Indels 0; Gaps DFYKIPIEIVNKTLPIVAITLLSLYYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQL 305	Application US/09323873A 6329503 FORMATION: Daniel E. Afar Rene S. Hubert Rene S. Hubert Rahan Leong Arthur B. Raitano Douglas C. Saffran Steve Chappell Mitchell INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF RENCE: 129.16USU2 PPLICATION NUMBER: US/09/323,873A ILING DATE: 1998-06-01 LICATION NUMBER: 60/087,520 ING DATE: 1998-06-30 SEQ ID NOS: 32 FastSEQ for Windows Version 4.0 Battle Told Now Sapiens Homo Sapiens 3a-8

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RESULT 2
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complete sequence. linear

Human BAC clone RG016J04 from AC002064 AC002064 AC002064.1 GI:2076723

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REFERENCE

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 156214)

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FEATURES source repeat repeat repeat repeat repeat repeat repeat	AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, sequence from more than one subcione; and the assembly was confirmed by restriction digest. MAPPING INPONMATION: The sequence of this clone was established as part of a maping and sequencing collaboration between the MRBRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center For additional information about the map position of this sequence, seremenhyriningov SOURCE INPONMATION: This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 93.785K. For references see: Shizuya et al., Proc. MRLI, Acad. Sci. VECTOR: PBELO Selection: chloramphenicol NEIGHBORING SEQUENCE INFORMATION: Actual start of this clone is at base position 1 of H_BGO16304. actual end is at 156214 of H_RGO16304. The orientation of this clone is unknown. This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:9454733). (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:91113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:9113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:9113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:9113580) and SWSS893 (NID:945473). This clone contains STS SWSS2784 (NID:9113580) and SWSS893 (NID:945473). This clone con	Gattung, S. and Maggi, L. The sequence of H. sapiens BAC clone RG016J04 Unpublished (1997) 2 (bases 1 to 156214) Waterston, R. Direct Submission Submitted (09-MAY-1997) Genome Sequencing Center Department of Genetics, Washington University St. Louis, MO 63108, USA http://genome.wustl.edu/gsc e-mail: sapiens@watson.wustl.edu NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.
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                                                 | acattttttttcctttattcctttgtcagagatgtgattcatccatatgctagaaaccaa | 1043
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                                       CAGAGTGACTTTTACAAAATTCCTATAGAGATTGTGAATAAAACCTTACCTATAGTTGCC 19540
                                                                             ACATTTTTTTCCTTTATTCCTTTGTCAGAGATGTGATTCATCCATATGCTAGAAACCAA 19480
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                                                                                                                                                                                                                                                                                      complement(51765.
/rpt_family="ALU"
complement(52252.
                                                                                                                                                                                                                                                                                                                      complement(51721.
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                           /rpt_family="THE"
complement(51124. .51156)
rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                      /rpt_family-"ALU"
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complement(41904.../rpt_family="Ll"
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/rpt_family="L1"
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40126. .40157
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99.8%;
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Pred. No. 2e-124;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                               Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: phrap; version 0.990319 consensus quality: 161010 bases at least 040 consensus quality: 161422 bases at least 030 consensus quality: 16152 bases at least 020 Insert size: 14300; agarose-fp Insert size: 162428; sum-of-contigs Quality coverage: 10.76x in 020 bases; agarose-fp Quality coverage: 9.47x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 162928)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Lect., Idol, J.R., Karlins, E., Laric, P., Lect., S.-O., McCloskey, J.C., McClowell, J., Pearson, R., Prasad, A., Stantripop, S., Malker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L., and Green, F.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NISC Comparative Sequencing Initiative Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Pan troglodytes clone RP43-120K11,
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                                                                                                                                                                                                                                                                                                                                                                                                        Center project Information
Center project name: ces
Center clone name: 120K11
                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear HTG 12-DEC-2001
WORKING DRAFT SEQUENCE, 6
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13923

13922: contig of 13922 bp in 14022: gap of unknown length

length

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confirmed by restriction digest.

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HSAC002064
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Best Local
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This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                        NOTICE: This sequence may not represent the entire insert of this sections once, or longer because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99aaggtcactgtaggtgtggattggaagtggagattttgccaaatccttgaccattcgac 459
                                                                                                                                                                                           Genome Sequencing Center
Department of Genetics, Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATTAGATGCGGCTATCATGTGGTCATAGGAAGTAGAAATCCTAAGTT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAGGTCACTGTAGGTGTGATTGGAAGTGGAGATTTTGGCGAAATCCTTGACCATTCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAY-1997)
                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                Waterston, R
                                                                                                                                                                                                                                                                               Gattung, S. and Maggi, L. The sequence of H. sapiens BAC clone RG016J04 Unpublished (1997)
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                       HTG
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                                                                                                                                                                                                                                                                                                                                                                                         numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSAC002064
                                                                                                                                                                         St. Louis, MO 63108, USA http://genome.wustl.edu/gsc
                                                                                                                                                           e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                       (bases 1 to 156214)
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J04 from 7q21, complete sequence.
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; Pred No. 2.3e-128;
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                             problems,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 978SK. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NID: 9454733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:
        complement (26832.
                                          complement(25561.
/rpt_family="L1"
                                                                                           complement(25113.
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                                                                                                                                                                                 complement(14777.
/rpt_family="L1"
15715. .15767
                                                                           rpt_family="L1"
                                                                                                                         /note="similar to
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/rpt_family="L1"
11666 .11687
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/db_xref="taxon:9606"
/chromosome="7"
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/note="similar to
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/note="similar to human EST R09227 (NID:g761150)
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/note="similar to human EST N59831 (NID:g1203721)
yz77a10.s1"
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/note="similar to human EST N52554 (NID:g1193720)
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z139902.r1"
27125. .27544
/note="similar to human EST AA151796 (NID:g1720491)
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/note="similar to human EST W31628 (NID:g1312688)
zb97c08.s1"
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/note="similar to
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/note="similar to human EST W32120 (NID:g1313113)
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	RESULT 3 AC104475/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Db 17441 G Qy 460 t Db 17501 T	Oy 340 g - Db 17381 G Oy 400 g		Query Match Best Local : Matches 22	repeat repeat repeat	repeat repeat	repeat
NISC Comparative Sequencing Initiative Unpublished 2 (bases 1 to 162928) Green,E.D. Direct Submission Submitted (12-DEC-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA	AC104475 AC104475 Pan troglodytes clone RP43-120K11, WORKING DRAFT SEQUENCE, 6 unordered pieces. AC104475 AC104	GGAAGGTCACTGTAGGTGTGATTGGAAGTTGTAGCAATTCCTTGACCATTCGAC 17500 ttattagatgcggctatcatgtggtcataggaagtagaaatcctaagtt 508	gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa 399	atattottggtgatottggaagtgtccgtatcatggaatcaatctctatgatgggaa 339 	tch 34.4%; Score 178; DB 9; Length 156214; al Similarity 99.6%; Pred. No. 7.5e-97; 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0	_region /rpt_family="L1" 5140551501 /rpt_family="ALU" _region /rpt_family="L1" /rpt_family="L1" _region complement(51751region /rpt_family="ALU" /rpt_family="ALU" _region complement(52252.	_region complement(505405079 _region complement(508405079 _region complement(508205098 _region complement(511245115	/rpt_family="L1" /rpt_family="L1" t_region 4610046516 /rpt_family="L1" t_region 4837048781 t_region 683704878750216)

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                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2453)
Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C., Faris, M. and Jakobovits, A.
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FIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVILDLLQLC
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Genome Sequencing Center
Department of Genetics, Washingto
St. Louis, Mo 63108, USA
http://genome.wustl.edu/gsc
e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG016J04;
actual end is at 156214 of H_RG016J04. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Mashington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gattung, S. and Maggi, L.
The sequence of H. sapiens
Unpublished (1997)
(bases 1 to 156214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9788K. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone contains STS sWSS2784 (NID:g1113580) and sWSS893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone is unknown
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complement(8071.
/rpt_family="ALU"
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complement(977...
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/rpt_family="L1"
                                                                              complement (9406.
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/rpt_family="ALU"
complement(37630.
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/note="similar to
yf26d05.r1"
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/note="similar to
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yv71e06.r1"
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/note="similar to
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/note="similar to
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/note="similar to
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11666. .11687
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Direct Submission
Submitted (12-DEC-2001) NIH Intramural Sequencing
Submitted (12-DEC-2001) NIH Intramural Sequencing
Servement Circle, Gaithersburg, MD 20877, USA
Grovement Circle, Gaithersburg, MD 20877, USA
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                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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AC104475.1 GI:17530717
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                                                                        * This record will be updated will as soon as it is available and be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Center clone name: 100K11
Center clone name: 100K11
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 161001 bases at least Q40
Consensus quality: 161422 bases at least Q30
Consensus quality: 161562 bases at least Q20
Insert size: 162428; sum-of-contigs
Quality coverage: 10.76x in Q20 bases; agarose-fp
Quality coverage: 10.76x in Q20 bases; agarose-fp
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Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                              Quality coverage: 9.47x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mouse@nhgri.nih
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13922: contig of 13922 bp in
14022: gap of unknown length
36248: contig of 22226 bp in
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CCGATGAGAAGGTCAGAGAGATATTTGTTTCTCAACATGGCTTATCAGCAGGTAC 121269
                             ccgatgagaaggtcagagagatatttgtttctcaacatggcttatcagcaggttc 1338
                                                                                                                                                                                                                                                  tacggcaccaagtataggagatttccaccttggttggaaacctggttacagtgtagaaaa 1223
                                                                                                                                                                                                                                                                                                                                                                                                                 attactttgctctccctagtatacctcgcaggtcttctggcagctgcttatcaactttat 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cagagtgacttttacaaaattcctatagagattgtgaataaaaccttacctatagttgcc 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acattttttttcctttattcctttgtcagagatgtgattcatccatatgctagaaaccaa 1043
                                                                                                                              CAGCTTGGATTACTAAGTTTTTTCTTCGCTGTGGTCCATGTTGCCTACAGCCTCTGCTTA 121324
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                                                                                                                                                        cagcttggattactaagttttttcttcgctatggtccatgttgcctacagcctctgctta 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAGTGACTTTTACAAAATTCCTATAGAGATTGTGAATAAAACCTTACCTATAGTTGCC 121504
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92269. .122036
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clone_end:SP6
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66293. .92168
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122137. .162928
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/db_xref="taxon:9598"
/clone="RP43-120K11"
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66192: contig of 29844 bp in length
66292: gap of unknown length
92168: contig of 25876 bp in length
92268: gap of unknown length
122036: contig of 29768 bp in length
122136: gap of unknown length
162928: contig of 40792 bp in length.
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TITLE
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1 (bases 1 to 172915)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Haghighi, P.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
HO, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O.,
HO, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,
Stantrippe, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Stantrippe, S., Thomas, P.J., Touchman, J.W.,
Trangeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Papio cynocephalus anubis clone RP41-167P22, WORKING DRAFT SEQUENCE, 4 unordered pieces. AC099742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-NOV-2001) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsurgeon,C., Vogt,J.L., Walker,M.A., Walker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green, E.D.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 172915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 130000; agarose-fp
Insert size: 172615; sum-of-contigs
Quality coverage: 12.58x in Q20 bases; agarose-fp
Quality coverage: 9.47x in Q20 bases; sum-of-conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 171178 bases at least Q40
Consensus quality: 171910 bases at least Q30
Consensus quality: 172236 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                         2439
2539
8134
8234
40379
40479
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Center clone name: 167P22
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                                                                                                                       Location/Qu
1. .172915
                          /organism="Papio cynocephalus anubis'
/db_xref="taxon:9555"
/clone="RP41-167P22"
                                                                                                                                                  2438: contig of 2438 bp in length 2538: gap of unknown length 8133: contig of 5595 bp in length 8233: gap of unknown length 40378: contig of 32145 bp in length 40478: gap of unknown length 172915: contig of 132437 bp in length coation/Qualifiers

    Summary Statistics

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                                                                                                                                                                                                                                                                                                        ggaaggtcactgtaggtgtgattggaagtggagattttgccaaatccttgaccattcgac 459
                                                                                                                                                                                                 tgggtaaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatcca 699
                                                                                                                                                                                                                                                                      GCCCTAAGAGCCTTAGTGAAACTTTTTTACCTAATGGCATAAATGGTATCAAAGATGCAA 83307
                                                                                                                                                                                                                                                                                                                                                                                                                          gccctaagagccttagtgaaacttgtttacctaatggcataaatggtatcaaagatgcaa 399
                                                                                                                                                                                                                                    TGGGTAAAATCCTGATTGATGTGAGCAATAACATGAGGATAAACCAGTACCCAGAATCCA 83607
                                                                                                AX106433
Sequence 214 from
AX106433
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 444)

Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
         cancer
                 Compositions
                                                                                         AX106433.1
                                                             Homo sapiens
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Similarity 97.6%;
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40479. .172915
/note="assembly_fragment"
a 31733 c 32277 g 56096
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8234 . 40378
/note="assembly_fragment
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2539. .8133
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clone_end:SP6
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                 and methods
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thods for therapy
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Sequence
AX140724
                                                                                                                               Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
                                                                         Patent: WO 0134802-A 214 17-MAY-2001; CORIXA CORPORATION (US)
                                                                                                                   Compositions and methods
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     Homo sapiens
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/db_xref="taxon:9606"
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/note="n = A,T,C or G"
a 100 c 78 g 143
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/organism="Homo sapiens"
/db_xref="taxon:9606"
100 c 78 g 14
                                                      Location/Qualifiers
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Sequence
AX200584
                                                                                                                                                                                               Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of p
                                                                                                                                                               Patent: WO 0151633-A 214 19-JUL-2001; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="taxon:9606"
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Sequence 214
AX267240
AX267240.1
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                       Patent: WO 0173032-A 214 04-OCT-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
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214 from Patent WO0173032.
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/db_xref="taxon:9606"
100 c 78 g 14
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                                                                                                                       Score 425.8; DB 6;
Pred. No. 1.1e-97;
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Day,C.H.,
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Lolettich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Larice, P., Lee-Lin, S.-Q., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Thomas, L., H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (24-MAR-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Oct 27, 2001 this sequence version replaced gi:7321458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, E.D.
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 205085)
                                                                                                                                                                                                                                                      Insert size: 197000; agarose fp
Insert size: 192000; pulse-field-gel
Insert size: 204185; sum-of-contlys
Ouality coverage: 9.35x in 020 bases; agarose-fp
Ouality coverage: 9.03x in 020 bases; pulse-field-gel
Ouality coverage: 9.03x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 199516 bases at least Q40
Consensus quality: 200596 bases at least Q30
Consensus quality: 201000 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: xh
Center clone name: 119M
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Qy 400 gga Db 186738 GGC	Qy 340 go	. Qy 280 as Db 186621 Ac	Query Match Best Local Matches 46	BASE COUNT ORIGIN	misc_f	misc_f	.misc_f	misc_f	misc_f		misc_fea	misc_f	misc_f	misc_f	misc_f			source	FEATURES												
gaaggtcactgtag CAGGTCACCGTGG	gccctaagagcctta GCCCTAAGAGCCT	ggatattettggtg 	21.7 Local Similarity 87.2 nes 463; Conservative	vect. 61131 a 40	eature 1533 /not	eature 1100	feature 81890.	eature 62111.	feature 4793		ture	feature 2284	feature 9654	feature 4529	feature 1	/clo /clo	/str /db_	1 /org	,	* 153236 * 153336	* 110020	818	* 62111 * 81790	* 62011	478	* * 33955 34055	228) 0 (* 4529 9554	* 4429	* be preserved
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ggagattttgccaa; 	cctaatggcataaa! CTAATGGCATAAA!	cgtatcatggaatca TCTACCATGGAATCO	Score 411; DB 2; Pred. No. 3.5e-93; Mismatches 65;	61026 t 91	agment	ragment"	ragment"	rragment"		ragment	agment"	agment	agment		+	9" ouse BAC library	090"	culus"	0 + 7 + 7	inknown leng	of 43216 bp in	of 28030	of 19679	anknown leng	unknown leng	unknown length of 13777 bp in	of 11108 bp in	of 1309	of 5025	unknown length	
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460 ttattagatgcggctatcatgtggtcataggaagtagaaatcctaagtttgcttctgaat 519

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TITLE
JOURNAL
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AUTHORS
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ORGANISM
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1 (bases 1 to 227144)

Äyele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Bouffard, G.G., Breen, K., Brinkley, C., Hooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S., Phomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-JUL-2001) NIH Intramural Grovemont Circle, Gaithersburg, MD 2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: phrap; version 0.990319
Consensus quality: 225678 bases at least Q40
Consensus quality: 225959 bases at least Q30
Consensus quality: 226087 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 225000; pulse-field-gel
Insert size: 225944; sum-of-contlys
Quality coverage: 12.84x in Q20 bases; agarose-fp
Quality coverage: 12.84x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                Center clone name: 261D18
                                                                                                                                                                                                                                                                                                                  Center project name: qv
                                                                                                                                                                                                                                                                                                                                                               Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                             Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov
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ne 5 clone RP23-261D18
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BASE COUNT
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Best Local Similarity
Matches 463; Conserv
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                                                               atgctgaatatttggcttcattattcccagattctttgattgtcaaaggatttaatgttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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109756. .227144
/note="assembly_fragment"
46378 c 46791 g 65638
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/note="assembly_fragment
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/strain="C57BL6/J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/chromosome="5"
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Pred. No. 3.6e-93;
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tcatgtggtagatgtcactcatcatgaagatgctctcacaaaaaacaaatataatatttgt
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Rattus no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steiner, M. S., Zhang, X., Wang, Y. and I. Growth inhibition of prostate cancer novel tumor suppressor gene, pHyde Cancer Res. 60 (16), 4419-4425 (2000)
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/product="tumor suppressor phyde"
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/db_xref="GI:12642829"
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GNRQVLICGDQLEAKHTVSEMARAMGETPLDMGSLASAREVEAIPLRLLPSWKVPTLL
ALGLSTQSYAKNFIRDVLQPYIRKDENKFYKMFLSVVNNTTIPCVAYVLLSLVYLLPGVL
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NLAVKQVLANKSRLWVEEEVWRHEISTYSLGVLALGMLSTLAVTSIPSIANSLNWKEES
FVQSTIGEVALMLSTWHTLTYGWTRAFEEHYKKFYLPTFTLTLLLPCVIILAKGLFL
LPCLSHRLTK.RRGWEENDGAVKFMLPAGHTQGEKTSHV"
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/strain="Dunning"
/db_xref="taxon:10116"
/cell_line="AT-1"
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Eutheria;
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             CCTCCTGCCCTGCCTCAGCCACAGACTCACCAAGATCCGCAGGGGGCTGGGAGAGG
                                        atteetteeatgtataageegaaagetaaaaegaattaaaaaaggetgggaaaag
                                                                                      accaaactttgttcttgctcttgtttttgccctcaattgtaattcttgggtaagattatttt
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                                                                                                                                                 tgttttaatttatggatggaaacgagcttttgaggaagagtactacagattttatacacc
                                                                                                                                                                                           GGAGTTCAGCTTTGTGCAGTCCACGCTGGGCCTTCGTGGCCCTGATGCTGAGCACAATGCA
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Patent: WO 0159127-A 18 16-AUG-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Tang,Y.T., Yue,H., Baughn,M.R., Yao,M.G., Bandman,O.,
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REFERENCE AUTHORS ACCESSION VERSION LOCUS DEFINITION RESULT 1 AY029585 KEYWORDS FEATURES REFERENCE SOURCE TITLE TITLE AUTHORS JOURNAL ORGANISM Direct Submission Submitted (10-APR-2001) University Hospital, 184 75012, France Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hon 1 (bases 1 to 1845)
Serru,V., Manivet,P., Lenoir,C., Eschwege,P., Lamblin,D. Vaubourdolle,M., Kellermann,O. and Loric,S. Dudulin 2, a new tumor antigen expressed in various huma Homo sapiens AY029585 Loric, S. and Serru, V. Unpublished Homo sapiens AY029585 (bases 'n /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="2" Location/Qualifiers 1 to 1845) GI:14017410 1845 dudulin 2 mRNA, 184 Biochemistry A Laboratory, Saint-Anto 4 rue du Faubourg Saint-Antoine, Paris bp mRNA complete cds. linear Saint-Antoine Euteleostomi; human PRI НОШО 09-MAY-2001

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EVQSSLGFVALVLSTLHTLTYGWTRAFEESRYKFYLPFTFTLTTLVPCVVILAKALFL
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                Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951) Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo capping; fis (full insert sequence). Homo sapiens teratocarcinoma cell_line:NT2 cDNA to clone_lib:NT2RP4 clone:NT2RP4001138.
                                                                                                                                                                                                                                  Unpublished (2000)
2 (bases 1 to 3912)
Isogai,T. and Otsuki,T.
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Homo sapiens cDNA FLJ10829 fis,
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Location/Qualifiers
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clone NT2RP4001138.
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source

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GNRQVPICGDQPEAKRAVSEMALÄMGFNPVDMGSLASAWEVEAMPLRLLPAWKVPTLL
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LPCISRRLARTRRGWBERESTIKFTLFDDHALAEKTSHV"

1148 c 1071 g 830 t
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/db_xref="GI:7023107"
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Pred. No. 1.3e-85;
0; Mismatches 571;
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Search completed: May Job time: 18694 sec 9 2002, 02:12:49

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1: /cgn2_6/ptodata/2,

2: //gn2_6/ptodata/2,

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US-09-651-941-17
US-08-724-974A-3
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US-08-482-855-2
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Best Local S
Matches 173
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                                                                                                                                                                                                                                                                  LENGTH: 17
TYPE: PRT
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les 173; Conserv
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Sequence 4, Appli	Sequence 3, Appli	-	Sequence 46, Appl	-	Sequence 46, Appl	Sequence 9, Appli	Sequence 1, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 2, Appli				

ALIGNMENTS

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Sequence 8, Application US/09323873A Patent No. 6329503
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APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SEPPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                   MSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRA 418
                                                                                        Conservative
                                                                                                                                                                                                                                                                         35.6%; Score 901; DB 4;
100.0%; Pred. No. 1.8e-85;
Live 0; Mismatches 0;
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APPLICANT: AITHUR B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.160302
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
INUMBER OF SEG ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEG ID NO 2
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lal, preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROSTATE
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                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLL 126
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APPLICATION
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                                                                                                                                                    USA
                Word Perfect 6.1 for Windows/MS-DOS 6.2
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US-09-083-521-1
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Best Local Similarity
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Patent No. 6329151
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Best Local Similarity
Matches 131; Conserv
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TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic FILE REFERENCE: BC1011 US NA CURRENT APPLICATION NUMBER: US/09/655,270A CURRENT FILING DATE: 2000-09-05 PRIOR APPLICATION NUMBER: 60/120,702 PRIOR FILING DATE: 1999-February-19
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 845-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LALVLPSIVIL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 LALVLPSIVIL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 LAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 MYHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL
                                 76 VTHHEDALTKTNIIFVAI----HREHYTSLWDLRHLLVGKILI------DVSNNMRIN 123
                                                                                          25 IKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFV 120
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                     1 MKSSKIAVVG--GTGPQGKGLAYRFAAAGWPVVIGSRSAERAEEAALEVRRRAGDGAVVS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL
AADNASAAADCPIILLVVPYDGHRELVS---ELAPIFAGKLVVSCVNPLGFDKSGAYGLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CERRONE, MICHAEL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.8%; ilarity 100.0%; Conservative 0
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0) 645-4166
) 845-4166
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                                                                                                                                                                                                                                                                                                                                                                                     UMBER: 60/120,702
1999-February-19
UMBER: 60/152,542
                                                                                                                                                              5.7%; Score 144.5; DB 4 28.0%; Pred. No. 5.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855-0555
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                                                                                                                                             33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                               DB 4;
                                                                                                                                               88;
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                                                                                                                                                                               Length
                                                                                                                                                                                   227;
                                                                                                         ---- VVD 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Rhodococcus erythropolis HL US-09-651-941-17
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                                                                                                                                                                                                                                                                 Sequence 2, Application US/08724974A Patent No. 5912335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09651941 Patent No. 6355470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,545
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RAINER, RUSS TITLE OF INVENTION: General File REFERENCE: BC1022 U
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APPLICANT: WALTERS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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ZIP: 19405-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
COMPUTER: IBM 486
                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         116 VEEGSAAEQLRDLVPGATVVAAFHHLSAVNLWEHE-GP--LPEDVLVCGDDRSAKDEVAR 172
                                                                                                                                                                                                                                                                                                                                                                                                        181 LARQLNFIP-IDLGSLSSAREIENLPLRLFTLWR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 QYPESNAEYLASLFPDSLIVKGFNVVSA---WALQLGPKDASRQVYICSNNIQARQQVIE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LARQLNFIP-IDLGSLSSAREIENLPLRLFTLWR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 QYPESNAEYLASLFPDSLIVKGFNVVSA---WALQLGPKDASRQVYICSNNIQARQQVIE 180
                                                                                                      STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VTHHEDALTKTNIIFVAI----HREHYTSLWDLRHLLVGKILI------DVSNNMRIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 IKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPH------VVD 75
                                                                                                                                                                                                                                                                                                                                                                       LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AADNASAAADCPIILLVVPYDGHRELVS---ELAPIFAGKLVVSCVNPLGFDKSGAYGLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKSSKIAVVG--GTGPQGKGLAYRFAAAGWPVVIGSRSAERAEEAALEVRRAAGDGAVVS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
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                                                                                         PΑ
                                                                                                                                                                                                          Derk J. Bergsma, Catherine E. Ellis
                                                                       USA
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BC1022 US NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 144.5; DB 4
28.0%; Pred. No. 5.8e-07;
                                                                                                                                                                                           HUVCT36
                                                                                                                        Beecham Corporation Road, P.O. Box 1539
                     3.5 INCH, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Mismatches 88;
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                       STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 227;
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US-08-724-974A-3 ; Sequence 3, Application US/08724974A ; Patent No. 5912335
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Best Local Similarity
Watches 57; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-724-974A-2
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Derk J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                  SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 KIILFLPCI--SRKLKRIKKGWEKSQFLEEGI 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 HVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 VADLFYICSLPFW------LQYVLQHDNWSHGDLSCQVCGILLYENIYI-SVGFLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 MYHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 IHQTLAPVVYVTVL----VVGFPANCLSLYFG-----YLQ--IKARNELGVYLCNLT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 VNKTL-PIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 HYPIQAWQRAI--NYYRFLVGFLFPICLLLASYQGILRAVRRSHGTQKSRKDQIQRLVLS 345
                                                                                                  COMPUTER:
                                                                                                                                                                                                                STREET: 709 SwedeLand CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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                                                                             OPERATING SYSTEM:
                                                                                                                     MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                ZIP: 19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVVIFLACFLPYHVLLLVRSVWEASCDFAKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAVTSIPSVSNALNWREFSFIQSTLGYVA-----LLISTF----
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                                                            WORDPERFECT 5.1
                                                                                                  IBM 486
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October 3, 1996
October 3, 1996
                                                                                                                                                                                                                                                                                                                                                Bergsma, Catherine E. Ellis
A No. 5912335el G-Protein
                                                                             WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                                                                                               HUVCT36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%; Score 118.5; DB 21.0%; Pred. No. 0.001; tive 46; Mismatches
                 US/08/724,974A
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                                                                                                                                                                                                                                           Road, P.O. Box 1539
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                                                                                                                                                                                                                                                                                                                                                  Coupled Receptor
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11;

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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; OTHER INFORMATION: STEAP-1 PEPTIDE US-09-323-873A-20
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                                                                                                                  SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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                                                                                                                                  PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
                                                                                                                                                                                                                                                                                              APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERVENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THI
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                       FEATURE:
                                                   ORGANISM: Artificial Sequence
                                                                                                 ENGTH:
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NAME: William T. Han
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 HYPIQAWQRAI--NYYRFLVGFLFPICLLLASYQGILRAVRRSHGTQKSRKDQIQRLVLS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 HVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 VNKTL-PIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 TVVIFLACFLPYHVLLLVRSVWEASCDFAKGV 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 IHQTLAPVVYVTVL----VVGFPANCLSLYFG------YLQ--IKARNELGVYLCNLT
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Amino Acid
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6329503
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US-08-487-886-2
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5744448
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Best Local Similarity 58.8%;
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TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOK AFFILION NUMBER: 07/6/U
APPLICATION NUMBER: 07/6/U
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
28546
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: US
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//8/487,886
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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                                  NAME/KEY: transmembrane domain LOCATION: 350 to 613 IDENTIFICATION METHOD: similar IDENTIFICATION METHOD: protein
                                                                                                                        IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                     NAME/KEY: signal sequence LOCATION: -17 to -1
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   NAME/KEY:
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GY: Linear
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Nugent, No. 5744448een Patrice
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                                                                                                                                                                              putative amino-terminal extracellular domain 1\ \text{to}\ 349
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putative transmembrane region
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Ares-Serono, Inc.
change Place, 37th floor
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                                                                                                                                                                                                                                   hydrophobic
                                    protein-coupled receptor transmembrane domains
                                                     similarity to other G
                                                                                                                        dimeric glycoprotein domains, hydrophilic
                                                                                                                                                             similarity with other
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Pred. No. 0.00025;
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                                                                                                                                           receptor extracellular
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US-08-487-886-2
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Best Local S
Matches 84
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                                            306
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                                                                                                              301 VDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFDYDLCNEVVDVTCSPKPDAFNPCEDIM
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IDENTIFICATION METHOD: similarity to other (IDENTIFICATION METHOD: protein-coupled receil DENTIFICATION METHOD: hydrophobic, about 20
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IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled rec IDENTIFICATION METHOD: hydrophobic, about
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 106; DB 1; Length 695; Local Similarity 16.4%; Pred. No. 0.031; res 84; Conservative 81; Mismatches 148; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                               ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEIRIEKANNL-LYINPEAFONLPNLQYLLISNTGIKHLPDVHKIHSLOKVLLDIQDNIN 156
                                        G-----LLSFFFAMVHVA-----
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				RESULT US-08- Sequ Fate Pate A A T T T C	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
NAME/KEY: putative amino-terminal extracellular domain LOCATION: 1 to 349 IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular IDENTIFICATION METHOD: domains, hydrophilic FEATURE: NAME/KEY: transmembrane domain LOCATION: 350 to 613	: 695 Amino acid SY: Linear TYPE: protein TYPE: signal sequence SN: -17 to -1 PICATION METHOD: hydrophobic	CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UNMER: 07/670,085 FILING DATE: 15-MAR-1991 ATTORNEY/AGENT INFORMATION: NAME: Williams, Stephan P. REGISTRATION NUMBER: 28546 REFERENCE/DOCKET NUMBER: US/252 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 723-1300 TELEPHONE: (617) 723-8923 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	STATE: MA COUNTRY: USA ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density COMPUTER: IBM PS/2, model 55 SX COMPUTER: IBM PS/2, model 55 SX OPERATING SYSTEM: MS-DOS version 4.0 SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/482,855 FILING DATE: 07-JUN-1995	SULT 10 -08-482-855-2 Sequence 2, Application US/08482855 Patent No. 6121016 GEMERAL INFORMATION: APPLICANT: Kelton, Christie Ann APPLICANT: Schweickhardt, Rene Lynn APPLICANT: Cheng, Shirley Vui Yen APPLICANT: Nugent, No. 6121016een Patrice TITLE OF INVENTION: Human Follicle Stimulating TITLE OF INVENTION: Hormone Receptor NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESSE: Stephan P. Williams, ADDRESSEE: Stephan P. Williams, ADDRESSEE: Ares-Serono, Inc. STREET: Exchange Place, 37th floor CITY: Boston	361 GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVPRPLMCNLAFAD 408 348 SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTL 398 349

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Local Similarity 16.4%;
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IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled receindentification method: hydrophobic, about 1
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IDENTIFICATION METHOD: similarity to other (IDENTIFICATION METHOD: protein coupled reception of the couple
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                                                                                                                                                                          Sequence 6, Application US/07757342D Patent No. 6218509
GENERAL INFORMATION:
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Best Local Similarity
Matches 45; Conserv
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REFERENCE/DOCKET NUMBER: SISK=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acid
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NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,
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MEDIUM TYPE: Floppy disk
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                                                                                                     MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                              APPLICANT: IGARASHI, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20004
CITY: Boston
STATE: Massachusetts
COUNTRY: US
                                              STREET: 130 Water Street
                                                                         ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 Seventh Street, N.W.,
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 97.5; D. Pred. No. 0.09339; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KILIDVSNNMR 121
                                                                          ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
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                                                                          B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                            213
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  RESULT 14
US-07-841-997A-2
; Sequence 2, Application US/07841997A
; Patent No. 5422254
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SEQUENCE DESCRIPTION: SEQ ID NO: US-07-757-342D-6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
511 MKVSICLP 518
                                                            433 V-LALVLP 439
                                                                                                               451 ASELSVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVLGWTFAFAAALFPIFGISSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ---FNGTQLDELNLSDNNNLEELPNDVFQGASGPVILDIS------RTKVHSLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                           344 NIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE-----FSFI
                                                                                                                                                                                                                                                                                                                                                 356 EDIMGYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVP-----RFLMCNLAFAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 ILRQDIDDMTQIGDQRVSLIDDEPSYGKGSDMMYNEFDYDLCNEVVDVTCSPKPDAFNPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 NQQSDFYKIPIEIVN--KTLP----IVAITLLSLVY-----LAGLLAAAYQLY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 HEIRIEKANNL-LYINPEAFQNLPSLRYLLISNTGIKHLPAVHKIQSLQKVLLDIQDNIN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG-------KILIDVSNNMR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                        QSTLG---YVALLISTFH----
                                                                                                                                                                                                                                                                                                                                                                                                        RKQLG-----LLSFFFAMVHVA------YSLCLPMRRSERYLFLNMAYQQVHA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGLENLKKLRARSTYRLKKLPNLDKFVTLMEASLTYPSHCCAFANLKRQISELHPICNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IH-----IVARNSFMGLSFESVILWL----SKNGIEEIHNCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/757,342D FILING DATE: 10-Sep-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 692 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 41226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7%;
                                                                                                                                                                                                                                  -LCIGIYLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVF 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 4
Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 142; Indels 194;
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                                                                                                                                                                              -VLIYGWKRAFEEEYYRFYTPPNF 432
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APPLICANT: Londes
APPLICANT: VIOTE
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TITLE OF INVENTION: A me
TITLE OF INVENTION: of o
TITLE OF INVENTION: stru
TITLE OF INVENTION: yeas
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LENGTH: 495 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34409
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/836,021
FILING DATE: February 14, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS
SOFTWARE: WP5.1 file exported as DOS text file
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Alko Ltd.
STREET: PO Box 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                             188
                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                       252
                                                                                                                                                                                                                                 195 ---RILPVRQEILKGVLSCDLVGFHTYDYARHFLSSVQRVLNVNTLPNGVEYQGRFVNVG 251
                                                                                                                                                                                                                                                                                                           137 TFTNEIAKTMNHNDLIWVHDYHLMLVPEMLRVKIHEKQLQNVKVGWFLH--TPFPSSEIY 194
                                   261 IVAITLLSLYYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYS 320
                                                                                                                                                                                                                                                                                                                                                                                      80 KDLLEKFNAVPIFLSDEIADLHYNGFSNSILWPLFHYHPGEINFD--ENAWFG-YNEANQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                          80 EDALTKTNIIFVAIHRE----HYTS-----LWDLRHLLVGKILIDVSNNMRINQYPESNA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Finland
                                                                                                                                                                                           --- IPIDLGSLSSARE----
FEELISLYAVSDVCLVSST - -
                                                                                                                                                     AFPIGIDVDKFTDGLKKESVQKRIQQLKETFKGCKIIVGVDRLDYIKGVPQKLHAMEVFL 311
                                                                                                                                                                                                                                                                     ICSNNIQARQQVIE--
                                                                         NEHPEWRGKVVLVQVAVPSRGDVEEYQYLRSVVNELVGRINGQFGTVEFVPIHFMHKSIP
                                                                                                             -----WRGPVV---VAISLATFFFLYSFVRDVIHPYARNQQSDFYK---IPIEIVNKTLP 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mary E. Gormley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helsinki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202)887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ondesborough, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide
                                                                                                                                                                                                                                                                                                                                              ----EYLASLFPDSLIVKGF-----NVVSAWALQLGPKDASRQVY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%; Score 89.5; DB
17.8%; Pred. No. 0.94;
tive 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of organisms by transforming them with the structural genes for the short and long chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yeast trehalose synthase
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                                                                                                                                                                                             ----IENLPLRLFTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                145;
-RDGMNLVSY ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 185;
-EYI 402
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80 EDALTKTNIIFVAIHRE----HYTS-----LWDLRHLLVGKILIDVSNNMRINQYPESNA 130

Query Match Best Local Similarity Matches 83; Conserv

Conservative

53;

Score 89.5; DB Pred. No. 0.94; 53; Mismatches 1

DB 1; 145;

Length 495; Indels 185;

Gaps

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3.5%; 17.8%;

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; MOLECULE TYPE: ; HYPOTHETICAL: US-08-290-301-2
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US-08-290-301-2
                                                                                                                                                                                                                                                                                                                                                                 CURRENT ATTACHMENT US/08/29U, 3U1
APPLICATION NUMBER: US/08/29U, 3U1
FILING DATE: 15 August 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FI 943133
FILING DATE: 29 June 1994
APPLICATION NUMBER: PCT/FF193/0004
FILING DATE: 15 February 1993
APPLICATION NUMBER: 07/841,997
APPLICATION NUMBER: 07/841,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5792921 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2,
                                                                                                                             TELEFAX: (202) 466-20
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mandel, Al
TITLE OF INVENTION: :
TITLE OF INVENTION: :
TITLE OF INVENTION: :
                                                                                                                                                                                                                                                                      AFFILING DATE: 28 February 1992
APPLICATION NUMBER: 07/836,02:
FILING DATE: 14 February 1992
ATTORNEY/AGENT INFORMATION:
NAME: KUDOVCIK, RONAID J.
                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: PC-DOS
SOCTWARE: WP5.1 file exported as DOS text file
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: Alko Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 LPDVKKEVNW-----EKLYKYISKYTSAF-----WGENFVHELY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 LCLPMRRSERYL--FLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTS 378
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 0//v--.
APPLICATION NUMBER: 0//v--.
FILING DATE: 28 February 1992
FILING TOWN NUMBER: 07.036,02
                                                                             TYPE:
                                                                                                                                                                                                        REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                              NAME: Kubovcik, Ronal
NAME: Lydon, James C.
                                                         TOPOLOGY:
                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette,
                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACQEEKKGSLILSEFTGAAQSLNGAIIVNPWNTDDLSD---
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                                                                           amino acid
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                                                                                            495 amino acids
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ALIGNMENTS

RESULT AAU10187 Human; Six-Transmembrane Protein of Prostate 1; STM;1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic. Key Human Six-Transmembrane Protein of Prostate 1, STMP1. WO200172962-A2 Domain Domain Domain 16-JAN-2002 AAU10187; AAU10187 standard; Protein; 490 Domain Domain Homo sapiens (first entry) /label= Transmembrane_domain_5 432..452 Location/Qualifiers 209..230 360..380 /label= Transmembrane_domain_(/label= Transmembrane_domain_4 /label= Transmembrane_domain_3 /label= Transmembrane_domain_2 /label= Transmembrane_domain_1 ..415 . 325 . 273 A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence represents a prostate specific protein, Six-Transmembrane Protein of Prostate 1, STM;1.
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                         testis-specific polypeptides and the nucleic acids encoding them. CC Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the CC transgenic animal expressing the nucleic acids, antisense molecules for detecting the nucleic acids, antisense molecules (for the nucleic acids and methods of isolating modulators of the CC proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cc proteins, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be cused include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The CC present sequence is prostate specific protein, Six-Transmembrane cover.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human six transmembrane epithelial antigen of CC the prostate (STEAP)-2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on CC chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian CC and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that CC expresses STEAP, or inhibiting growth or killing cells expressing STEAP, or inhibiting growth or killing cells expressed STEAP, or inhibiting growth or killing cells expressing STEAP, or inhibiting the patient with a cancer that CC comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, CC such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly.
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Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the protein acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis concertific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign constatic hyperplasia, acute prostatitis, testicular cancer, prostatic hyperplasia, acute prostatitie, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence is prostate specific protein, Six-Transmembrane
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                         80.3%;
99.7%;
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                         Score 2036; DB 22;
Pred. No. 8.6e-207;
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                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                               The invention relates to isolated polynucleotide polypeptide (II) sequences. (I) is useful as hybr
                                                        Claim
                                                                                                                                        Drmanac RT,
                                                                        biodiversity
                                                                                                                N-PSDB;
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23-AUG-2000;
                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                       (HYSE-) HYSEQ
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                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                      ABG12306 standard;
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DB; AAS76493.
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upplement; medical imaging; diagnostic; genetic
                                                        SEQ
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                               tide (I) and hybridisation probes
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tage for identifying expressed genes. (I) is useful in gene therapy techniques.

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Note: The sequence data for this patent did not appear in the printed appear in the pr
                   WO200175067-A2
                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                    ABG00113 standard;
                                                       Homo sapiens
                                                                                                                                                 Novel human diagnostic protein #104.
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                                                                                           imaging;
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maging; diagnostic; genetic (
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Pred. No. 8.6e-199;
0; Mismatches 1;
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                                                                                                           forensic;
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The control of control of the control of 
                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, for responsible for
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23-AUG-2000;
                                                                                                                   Sequence
                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 30472; 103pp; English.
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DB; AAS64300.
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77.4%;
87.4%;
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                               DB 22;
                               Length 1273;
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Matches 313 181 193 301 253 121 133 61 Local 1 MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE ringypesnaeylaslfpdslivkgfnvvsawalqlgpkdasrqvyicsnniqarqqvie rnpkfaseffphvvdvthhedaltktniifvaihrehytslwdlrhllvgkilidvsnnm RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM 388; Similarity Conservative Score 1962.5; Pred. No. 2.9e 0; Mismatches .9e-198; Indels 55; Gaps 300 360 372 312 240 252 180 120 132 60 1;

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RESULT AAEBC2841 ID AAEBC284 AAEBC
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                      The present sequence is an alternative version of human six transmembrane epithelial antigen of the prostate (STEAP)-2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and the comprises the variable domains of the heavy and the comprises the variable domains of the heavy and the comprises the variable domains of the heavy and the comprises the variable domains of the heavy and the comprises the variable domains of the heavy and the comprises the variable domains of the comprises the variable domains of the heavy and the comprises the variable domains of the heavy and the comprises the variable domains of the comprises the variable domains of the patient comprises the variable domains of 
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WPI; 2001-032016/04
N-PSDB; AAC89167.
                             Steiner MS,
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Note: This sequence is stated to be the same as that being shown as SEQ ID NO:8 (AAED2781) in figure 9A-9C of the specification. However the present sequence lacks several amino acids at its N-terminal end and has additional amino acids at its N-terminal end the sequence shown in figure 9A-9C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                  Drug metabolizing enzyme; DME; immunosuppressive; hepatotrophic; antiallergic; antiasthmatic; antib antisense therapy; gene therapy; human.
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Best Local Similarity 53.3
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17-FEB-2000;
25-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides human drug metabolizing enzymes (DME) and polynucleotides encoding the DMEs. The DME can be expressed by star recombinant methodology. DMEs and their agonists and antagonists are useful for the diagnosis, treatment, and prevention of autoimmune/inflammatory, cell proliferative, developmental, endocrine such as aneurysm, eye, metabolic, and gastrointestinal disorders, including disorders and infection. The present sequence represents a human DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide encoding a drug metabolizing enzyme useful for the diagnosis, treatment, and prevention of autoimmune/Inflammatory, cell proliferative, developmental and endocrine disorders -
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53.3%;
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Pred. No. 6.2e-135;
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Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or treat disorders specific polypeptide are useful to diagnose, prevent or treat disorders prostatic hyperplasia, acute prostatitis, testicular cancer, benign cryptorchidism, undescended, retractile, ascending or vanished testis; Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, The present sequence is a prostate specific protein, Six-Transmembrane
                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, compr prostate-specific or testis-specific nucleic acids
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                                                                                                                                                            Sequence
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Pred. No. 1.3e-134;
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19-JUL-2000;
31-AUG-2000;
04-DEC-2000;
 WPI; 2001-442255/47
                                                                                                                                                                                                                                                                                                                                                           Human; G-protein coupled receptor like protein; GPCR; immunogen; ophthalmic disease; neurological disease; Alzheimer's disease; Parkinson's disease; immunological disorder; HIV; candidiasis; human immunodeficiency virus; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; platelet disorder; systemic lupus erythematosus; rheumatoid arthritis; platelet disorder;
                          Yamazaki V,
Asundi V, I
                                                                                                                                                                                                                                                                                                          septic shock; systemic inflammatory response syndrome; SIRS; hormonal dysfunction; cancer; atherosclerosis; wound; STRAP-1; tissue regeneration; haemophilia; leukaemia; reperfusion injur
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                                                                                                                                                                                                                                                                                                                                                thrombocytopaenia; aplastic anaemia; inflammatory disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10;
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The present invention describes primer sets for synthesising 5602 (c) full-length cDNAs defined in the specification. Where a primer set (c) comprises: (a) an oligo-dT primer and an oligonucleotide complementary (c) to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end (c) sequence and an oligonucleotide comprises a 1-east 15 nucleotides and the combination of coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in c) the specification. The primer sets can be used in antisense therapy and comparise therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also which the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and C canabs9893 represent human clud sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; AAB92446 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
                              Query Match
Best Local Similarity
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11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                  Sequence
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l.3e-134;
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Otsuki
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29-APR-1999;
26-NOV-1999;
  regression of tumour apoptosis caused by (
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ctal; pancreatic;
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sor gene; DNA repair; cancer; melanoma; lymphoma
ncreatic; breast; brain; gastric carcinoma.
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14-AUG-2000; 22-FEB-2001

2000WO-US22315

WO200112662-A2

sapiens

epilepsy; diarrhoea

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RESULT 14
AAB74715
ID AAB7477
XX AAB7477
XX 12-JUN
DT 12-JUN
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DT Human
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KW antiar
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                            Human; membrane associated protein; MEMAP; diagnosis; cytostatic; antiinflammatory; anticonvulsant; membranesuppessive; antidiarrheic; antiarteriosclerotic; gene therapy; cell proliferative disorder; autoimmune disorder; inflammatory disorder; neurological disorder;
                                                                                                autoimmune disorder; infla
gastrointestinal disorder;
                                                                                                                                                                                      12-JUN-2001
                                                                                                                                                                                                            AAB74715;
                                                                                                                                                                                                                                  AAB74715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of DNA repair with the upregulation of apoptosis as the result of damage and the failure to repair DNA. The present sequence may be treat cancer, preferably melanoma, lymphoma, leukaemia, prostate, colorectal, pancreatic, breast, brain or gastric carcinoma.
                                                                                                                                                                   Human membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                        476
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                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                   associated
                                                                                                                                                                                                                                                                                        485
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                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                protein MEMAP-21
                                                                                                  cancer;
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                                                                                                                                                                                                                                  A
                                                                                                  inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC MEMAPS and agonist of MEMAPs can be used to treat a disease or condition coveracy restored with decreased expression of functional MEMAP and antagonists of MEMAP are used to treat a disease or condition associated with coveracy restored of functional MEMAP. These disorders include cell coveracy restored to the MEMAP polynucleotides and proteins are also used for the cdisorders. The MEMAP polynucleotides and proteins are also used for the cdisorders. The MEMAP polynucleotides and proteins are also used for the cdisorders. The MEMAP polynucleotides and proteins are also used for the cdisorders. The MEMAP polynucleotides and proteins are also used for the conclude cancer, inflammation, atherosclerosis, epilepsy and diarrhoea. CC MEMAP proteins can be used to screen for compounds which specifically concludes and mathematical concerning human con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEMAP) given in AAB74695 to AAB74731. MEMAPS have cytostatic, antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic antiarteriosclerotic activities, which can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1999;
09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF81741 to AAF81777 encode the human membrane associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lal P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LSETC---LPNGINGIKDARKYTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEF
                                                                                                                                                                                                                                                                                                  AEYLASLEPDSLIVKGENVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNEIP
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                                             FFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLG
                                                                                          IPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLS
                                                                                                                                                                                  \verb|mdqgslmaakeiekyplqlfpmwrfpfylsavlcvflffycvirdviypyvyekkdntfr|
                                                                                                                                                                                                          IDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYK
                                                                                                                                                                                                                                                                           aeylahlvpgahvvkafntisawalqsgaldasrqvfvcgndskakqrvmdivrnlgltp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 134-135; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459
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erson C;
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Pred. No. 1.
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l.8e-113;
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                                         composition to the patient. Treating a patient with a cancer that composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly.

Note: The present sequence is stated as being the same as that shown as SEQ ID NO:10 (AABD0236) in sequence listing of the specification. However
                                                                                                                                                                                                           The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP) 3 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-3; STEAP-3; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2000; 2000WO-US33040
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                                                                                                                                                                                                                                                                                                                                                                                                     proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          six transmembrane epithelial antigen of prostate (STEAP)-3 protein.
                                                                                                                                                                                                                                                                                                                                                    36; Fig 10A-10B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD07073.
                                                                                                                                                                                                                                                                                                                                                                                                   (six transmembrane epithelial antigen of the prostate) expressed in human cancers, useful for detecting and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hubert RS,
A;
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Query Match
Best Local Similarity
Matches 214; Conserv

Conservative

95,

Score 1155; D. Pred. No. 2.3e 95; Mismatches

DB 22;

459;

Indels Length

6

Gaps

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45.6%;

Sequence

459

AA;

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178
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Search completed: May 9, 2002, 02:12:49 Job time: 13406 sec ρy

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

May 9, 2002, 02:06:16; Search time 50.39 Seconds (without alignments)
934.387 Million cell updates/sec

Title:
Perfect score: US-09-802-520-1
Perfect score: 2534
Sequence: 1 MESISMMGSPKSLSETCLPN.....LEEGIGGTIPHVSPERVTVM 490

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ō,	υ	4	ω	2	1	Result No.
106	106.5	106.5	107	107.5	108	109	109	109	109	110	110.5	111.5	112.5	112.5	114.5	116	116.5	119.5	120.5	121	121.5	133	142	142	147	156.5	159.5	160	Score
4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.4	4.4	4.5	4.6	4.6	4.7	4.8	4.8	4.8			•		6.2		6.3	Query
695	1695	442	1769	202	712	1301	1184	694	320	695	222	1228	1034	365	361	198	242	216	232	191	629	223	224	212	213	239	211	198	Length
ب	N	N	2	N	N	N	Ŋ	N	N		ν	Ν	N	Ν	N	Ν	N	2	Ν	N	2	N	2	N	N	N	N	ν	BB
QRHUFT	JE0084	в64582	S53378	в83059	S50969	D85188	H71436	JC4301	T28379	JN0898	B84410	S59681	T30331	S68208	JC5653	AB3182	G82642	T00121	A69131	F86826	S60385	D64487	T10120	D69361	н69400	T50571	AC2560	D95285	ID
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ALIGNMENTS

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Qy 197 SAREJENLPLRLFTLWRGPVVVAISL 222 :: :	QY 139 DSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLS 196 :	Qy 88 IIFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFP 138 :: : : : : : : : : :	Qy 32 TVGVIGSGDFAKSLTIRLIRCGYHVVI-GSRNPKFASEFFPHVVDVTHHEDALTKTN 87 : : : : : : : : : : : :	Ouery Match 6.3%; Score 160; DB 2; Length 198; Best Local Similarity 26.7%; Pred. No. 2.6e-05; Matches 55; Conservative 40; Mismatches 83; Indels 28; Gaps 8;	RESULT 1 D95285 Conserved hypothetical protein SMa0349 [imported] - Sinorhizobium meliloti (strain 10 c; Species: Sinorhizobium meliloti 24-Aug-2001 #text_change 30-Sep-2001 C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #sequence_revision 25-Bis City

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Б
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C; Date:
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                                                                                                                                                                                                                                                                                                                                                                 A; Note: SCC75A.
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-239 <RED>
A;Cross-references: EMBL:AL133220; PIDN:CAB61708.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: A set of ordered cosmids and a detailed genetic and physical map for the A;Reference number: Z20556; MUID:97000351
A;Accession: T50571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, Microbiol. 21, 77-96, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-211 <KUR>
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C;Species: Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
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Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120;
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                   Matches
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Best Local Similarity 24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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23
                                                                    25 IKDARKVTVGVI-GSGDFAKSLTIRLIRCGYHVVIGSR----NPKFASEFFPHVVDVTHHE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 VIFLATPFTANQAALAEVGDLS----GKILVDCTNPVGVNLTHGLKSEQSGSELVQSFVP
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                                                                                                                                                                                                                                                                                                                                                                                                                    SCC75A.08c
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LPDVSGLVVGVLGGTGPQGKGLAYRLAKAGQKVIVGSRAAERAAAAAEEIGHGVEGADNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPIDLGSLSSAREIENLPLRLFTLW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSLIVKGFNVVSAWALQLGPKDASRQVY------ICSNNIQARQQVIELARQLNF 187
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                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein MJ1501
                                                                                                                                                                                                 6.2%;
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Pred. No. 3.1e-05;
                                                                                                                                                  Score 156.5; DB 2;
Pred. No. 6.2e-05;
il; Mismatches 72;
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                 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.I. Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P. Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, A; Reference number: A69250; MUID:98049343
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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing.arch A;Reference number: A69250; MUID:98049343
A;Accession: H69400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-213 <KLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein AF1209 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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179
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                                                                                                                                                                                                                                     89 IFVAIHREHYTSLWD-------LRHLLVGKILID-------VSNNMRINQYPE--SNAE 131
                                                                                                                                                                                                  67 -- VAV---- FTIPWEFAFDTAEMLKRQLAGKVVISPLVPMKKVGDNF-VYVRPEEGSAAE 119
                                                                                                                                                                                                                                                                                                                                                      37 GSGDFAKSLTIRLIRCGYHVVIGSRN----PKFASEFFPHVVDVT----HHEDALTKTNI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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                                               DLGSLSSAREIENL-PLRLFTLWR 213
DAGGLSNAHLVESLTPLILNVMKR
                                                                                                 KLASVLEESSVVAAYHSIPARRFANLGEEFEWDVPICGDS-GAKEVVVDLTEKISGLRAL
                                                                                                                                                                                                                                                                                                      GTGNLGEGLALRWGKLGYETIVGSRKLEKAEKLASDYLKKVGDASIIGMRNEDAAETCD- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAAALLPDSRVAAAFHHLSAVLLQDPEIDEIDTDVMVLGEERADVEI-----VQA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IELARQLNFIP----IDLGSLSSAREIENLPLRLFTLWR 213
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56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 147; DB 2;
27.5%; Pred. No. 0.0003;
tive 44; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

conserved hypothetical protein AF0892 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999

C; Accession: D69361

G

A; Molecule type:

DNA

;Status: preliminary; nucleic acid sequence not shown;

translation

not shown

P.;

Kaine, B.P.;

Sykes, arch

sulfate-reducing

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RESULT
D64487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: F420H2:NADP Oxidoreductase from Methanobacterium thermoautotrophicum: A;Reference number: Z16959; MUID:99037734
A;Recession: T10120
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-224 < HERP-
A;Cross-references: EMBL:Y17210
A;Experimental source: strain Marburg
C;Superfamily: conserved hypothetical protein MJ1501
C;Keywords: oxidoreductase
hypothetical protein MJ1501 - Methanococcus jannaschii C;Speckes: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change C;Accession: D64487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
T10120
F420-dependent NADP reductase (EC 1.6.8.-) - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T10120
C;Accession: T10120
R;Berk, H.; Thauer, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-212 <KLE>
A;Cross-references: GB:
C;Superfamily: conserve
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EBS Lett. 438, 124-126, 1998
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Best Local
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                                                                                                                                                                                             IDLGSLSSAREIENLPLRLFTL
                                                                                                                                                                                                                                                                                                                                                      ---IIFVAIHREHYTSLWDLRHLLVGKILIDV-----SNNMRINQYPESNAEYLA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTK--TN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IENLPLRLFTLWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFVAIHREH-YTSLWDLRHLLVGKI----LIDVSNNMRINQY--PESNAEYLASLFPDSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGDFAKSLTIRLIRCGYHVVIGSRNPK----FASEFFPHVVDVT----HHEDALTKTNI
                                                                                                                                                                                                                                    RFLEDQGTRVAAAFNNISASALLDITGPVDC--DCLIASDHRDALDLASELAEKIDGVRA 184
                                                                                                                                                                                                                                                                        SLFPD--SLIVKGFNVVSAWALQ--LGPKDASRQVYICSNNIQARQQVIELARQLNFI-P 189
                                                                                                                                                                                                                                                                                                                 EVAILTVPLQAQMAT-LGSVKEAIKGKVLIDATVPIDSCLGGSAVRYIDLWDGSAAERAA
                                                                                                                                                                                                                                                                                                                                                                                           GTGDQGLGLALRLALAGEEVIIGSRDAEKAVSAAQKVLEIAERDDLKVKGATNAEAAEEA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVLTIPWEHAIDTARDLKNILREKIVVSPLVPVSRGAKGFTYSSERSAAEIVAEVLESEK 127
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                                                                                                                                                          IDCGGLENARVIEKITPLLINL
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49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%;
29.2%;
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25.4%;
                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142; DB 2;
Pred. No. 0.0008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 142; DB 2;
Pred. No. 0.00074;
4; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
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A:Map position: 15L
C;Keywords: transmembrane protein
C;Keywords: transmembrane #status predicted
F;50-66/Domain: transmembrane #status predicted
F;125-141/Domain: transmembrane #status predicte
F;157-173/Domain: transmembrane #status predicte
F;240-258/Domain: transmembrane #status predicte
F;266-282/Domain: transmembrane #status predicte
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-629 <ARI>
A; Cross-references: EMBL: 274894; NID: g1420058; PID: e251928;
A; Cross-references: Strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z48239; NID:g1163073; PIDN:CAA88276.1; PID:g886945 R;Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
C;Accession: S60385; S66849; S57673
R;Casamayor, A.; Aldea, M.; Casas, C.; Herrero, E.; Gamo, F.J.; Lafuente, M. Yeast 11, 1281-1288, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus A;Reference number: A64300; MUID:96337999
A;Accession: D64487
                                                                                                                                                                                        A; Gene: SGD: FRE7
A; Cross-references:
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A:Map position: REV1473617-1472946
C;Superfamily: conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-629 < CAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: DNA sequence analysis of a 13 kbp
A; Reference number: S60385; MUID:96132030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable membrane protein YOL152w - yeast (Saccharomyces cerevisiae) N; Alternate names: hypothetical protein AOB629; hypothetical protein OO443
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A; Residues: 1-223 <BI
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                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
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Best Local :
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21.9%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.J.; Lafuente, M.J.;
                                                                                                                                                                                                                                                                                     PID:g1420059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
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RESULT 10
A69131
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A; Molecule type: DNA
A; Residues: 1-191 <570>
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A;Experimental source: strain IL1403
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Matches 47
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; Pred. No. 0.1;
55; Mismatches
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hypothetical protein 8 - Leptospira interrogans C;Species: Leptospira interrogans C;Species: Laptospira interrogans C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000 C;Accession: T00121 C;Accession: T0121 R;Takahashi, Y.; Akase, K.; Hirano, H.; Fukunaga, M. Gene 215, 37-45, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000811; GB:AE000666; NID:g2621287; PIDN:AAB84754.1; A;Experimental source: strain Delta H C;Genetics:
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A;MoLecule type: DNA
A;Residues: 1-216 <TAK>
A;Residues: 1-216 <TAK>
A;Cross-references: EMBL:AB010203; NID:g2780763; PIDN:BAA24368.1; PID:g27A;Experimental source: strain Ictero No.1; substrain icterohaemorrhagiae
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T00121
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A;Start codon: TTG
C;Superfamily: conserved hypothetical protein MJ1501
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A;Recession: A69131
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated A;Molecule type: DNA
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A; Title: Physical and
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A; Residues: 1-232 <MTH>
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Best Local Similarity
Matches 47; Conserva
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nes 49; Conserv
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                                                                                                                                     IGILGSGIVGQTLANGFLKYGAEVKIGTRDFGKLKDWLAKAGAGASIGSFSEAANFGEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEYLASLF - - - PDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDAAASADVVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS
                                             VLCSKGSVASEVLTLSGIDSLNGKTIIDTTNPISEIPPQNGVLNFFTSYNESLMEKLQKQ 125
                                                                                    FVAIHREHYTSLWDLRHL--LVGKILIDVSNNMR------INQYPESNAEYLASL 136
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                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                       Score 119.5; DE Pred. No. 0.045; 7; Mismatches
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Conserved hypothetical protein XF1737 [imported] - Xylella fastidiosa (Strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82642
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Tille: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20355717
A;Rote: for a complete list of authors see reference number A59328 below
A;Accession: G82642
A;Status: prellminary
A;Accession: G82642
A;Coss-references: GB:AED03997; GB:AED03849; NID:99106805; PIDN:AAF84546.1; GSPDB:GN001
A;Experimental source: strain 9a5c
A;Cross-references: GB:AED03997; GB:AED03849; NID:99106805; PIDN:AAF84546.1; GSPDB:GN001
A;Experimental source: strain 9a5c
B;Canargo, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Bueno, M.R.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Laigr
Chado, M.A.; Madeira, A.M.F.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Maceira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Myaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
M.; Tsubako, M. H.; Vallada, H.; Van Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
A;Genetics:
A;Gene: XF1737
conserved hypothetical protein Atu5183 [imported] - Agrobacterium tumefacien C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AB3182 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S.
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                        Wood, G.E.; Chen,
I.; Levy, R.; Li,
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C;Superfamily: G protein-coupled receptor 4
C;Keywords: glycoprotein; phosphoprotein
F;24-46/Domain: transmembrane #status predicted <TM1>
F;88-79/Domain: transmembrane #status predicted <TM2>
F;98-717/Domain: transmembrane #status predicted <TM4>
F;137-159/Domain: transmembrane #status predicted <TM4>
F;189-207/Domain: transmembrane #status predicted <TM6>
F;229-253/Domain: transmembrane #status predicted <TM6>
F;229-253/Domain: transmembrane #status predicted <TM7>
F;38-729/Domain: transmembrane #status predicted <TM7>
F;38/52/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;314,218,293,313/Binding site: phosphate (Thr) (covalent) (by protein kinase of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JC5653
G protein-coupled receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 21-Ju1-2000
C;Accession: JC5653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Ferrer-Martinez, A.; Felipe, A.; Mata, J.F.; Casado, F.J.; Pastor-Anglada, Biochem. Biophys. Res. Commun. 238, 107-112, 1997
A;Title: Molecular cloning of a bovine renal G-protein coupled receptor gene A;Reference number: JC5653; MUID:97445134
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A; Residues: 1-361 <FE
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oo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan,
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22.7%; Pred. No. 0.076;
tive 41; Mismatches 81
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Score 114.5; D: Pred. No. 0.21; Mismatches
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233 TVVIFLACFLPYHVLLLVRSVWEASCDFAKGV 264
                                                                             446 KIILFLPCI--SRKLKRIKKGWEKSQFLEEGI 475
                                                                                                                                                                   175 HYPIQAWQRAI--NYYRFLYGFLFPICLLLASYQGILRAVRRSHGTQKSRKDQIQRLVLS 232
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PRE1_YEAST
PHSC_ECOLI
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Science 273::058-1073(1996).

Science 273::058-1073(1996).

-i-FUNCTION: CATALYSES THE REDUCTION OF F420 WITH NADP(+) AND THE REDUCTION OF NADP(+) WITH F420H(2). PROBABLY COUPLES THE NADP-DEPENDENT OXIDATION OF THE ALCOHOL TO THE ALDEHYDE WITH DE F420-DEPENDENT REDUCTION OF CO(2) TO METHANE (ANABOLIC FUNCTION) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative F420-dependent NADP reductase (EC 1.-...
MJ1501.
                                                                                                                                                                            use
                                                                         Hypothetical
                                                                                                                                                                                            the
                                                                                                                                                                                                                         This
                                                           SEQUENCE
                                                                                                                                                 entities
                                                                                                                                                                                                           between
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Archaea; Euryarchaeota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2190;
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                                                                                                                                  send
                                                                                                                                                                                         ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                  COENZYME F420.
SIMILARITY: TO
                                                                                                                                                                                                                                                                             SIMILARITY).
CATALYTIC ACTIVITY: NADPH +
                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIIGKI
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                                                                                                                                  an
                                                                                                                non-profit institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for commanderes a license agreement (See http://www.isb-sib.ch/anman email to license@isb-sib.ch).
                                                          l protein; Oxidoreductase; NADP; Com
223 AA; 24068 MW; 2370BBD6F5BBD3D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                  TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE.
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 Score
Pred.
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                                                                                                                                                                                                                                                                               COENZYME F420 = NADP(+) + REDUCED
 133; DB 1;
No. 0.013;
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                                                                                                                                            (See http://www.isb-sib.ch/announce/
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03D9 CRC64;
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FRE7_YEAST
ID FRE7_YEAST
AC Q12333;
DT 15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Casamayor A., Aldea M., Casas C., Herrero E., Gamo Lafuente M.J., Gancedo C., Arino J.;
"DNA sequence analysis of a 13 kbp fragment of the chromosome XV containing seven new open reading fray Yeast 11:1281-1288(1995).

1 CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) +
1- COFACTOR: FAD (PROBALE).
1- SUBCELLULAR LOCATION: Integral membrane protein
1- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomyc
Saccharomycetales; Saccha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chelate reductase FRE7 OR YOL152W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ferric reductase transmembrane component 7 (F
                                                                                                                                                                                                                                                                                                     Oxidoreductase; Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / FY1679;
MEDLINE=96132030; PubMed=8553699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                 Pfam; PF01794; Ferric_reduct; 1.
                                                                                                                                                                                                                                                                                                                                                   L; Z48239; CAA88276.1;
L; Z74894; CAA99174.1;
; S0005512; FRE7.
erPro; IPR002916; Ferri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNLEKSRIIEAIT - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     Glycoprotein;
369 375
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Ascomycota; Saccharomycotina; Saccharomycetes;
; Saccharomycetaceae; Saccharomyces.
     128
128
188
215
258
258
286
286
313
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313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       license agreement (See http://www.isb-sib.ch/announce/
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  (POTENTIAL).
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RESULT 4
F4RE_METTH
ID F4RE_M
AC 026350
DT 15-DEC
DT 16-OCT
DT 16-OCT
DE PUTATI
GN MTH248
OS Methan
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RN [1]
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

-I-FUNCTION: CATALYSES THE REDUCTION OF F420 WITH NADP(+) AND THE REDUCTION OF NADP(+) WITH F420H(2). PROBABLY COUPLES THE NADP-DEPENDENT OXIDATION OF THE ALCOHOL TO THE ALDEHYDE WITH DE F420-DEPENDENT REDUCTION OF CO(2) TO METHANE (ANABOLIC FUNCTION) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum delitat. finational applications of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O26350;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DELTA H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative F420-dependent NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F4RE_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 AVKGYLRPGRSFMASTIANVSIVGE-----GCVELIVKDVEMAYSPGQHIFVRTIDKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
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                                                                                                                                                                                                                                                                                                   SIMILARITY: TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
CATALYTIC ACTIVITY: NADPH +
                                                                                                                                                                                                                                                                                                                                   COENZYME F420
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      AE000811; AAB84754.1;
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Best Local
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                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
An S., Goetzl E.J.;
Submitted (OCT-1995)
                                                                           GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Oxidoreductase; NADP; Complete proteome SEQUENCE 232 AA; 24539 MW; AlCE60ABC8474296 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ORPHAN RECEPTOR.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: FOUND IN MANY TISSUES, INCLUDING
TESTIS, PERIPHERAL BLOOD LEUKOCYTES, BRAIN, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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U35398; AAA79060.1;
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                                                                                GCR_1960; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casey G.
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                                                                                                         GCR_1937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETECTABLE IN OVARY.
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Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a novel G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Ovarian
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MIM; 601404;

InterPro;

PF00001; 7tm_1;

IPR000276;

GPCR_Rhodpsn.

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Best Local Similarity
Matches 57; Conser
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P32212;
01-OCT-1993
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DOMAIN
TRANSMEM
TISSUE=Testis;
TISSUE=Testis;
MEDLINE=94071854; PubMed=7504463;
Gromoll J., Dankbar B., Sharma R.S.,
Gromoll J., Cloning of the testicular
                                                                      Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Prim
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
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DOMAIN
                                                                                                                receptor).
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16-OCT-2001
                                                                                                                                                                                             MACFA
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TRANSMEM
                                                              NCBI_TaxID=9541;
                                                                                                     Macaca
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s; PS00237;
s; PS50262;
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(Rel.
(Rel.
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140
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37; G_PROTEIN_RECEP_F1_2; 1.
52; G_PROTEIN_RECEP_F1_2; 1.
1ed receptor; Transmembrane; G.
21 EXTRACELLULAR ()
                                                                                                                                                                                   STANDARD;
                                                                                                                                          27,
27,
40,
                                                                                           (Crab eating macaque) (Cynomolgus monkey) Chordata; Craniata; Vertebrata; Euteleost
                                                                                 Primates; Catarrhini;
                                                                                                                              , Last sequence update)
, Last annotation update)
hormone receptor precursor (FSH-R) (Follitropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41076 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               4.78;
                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

G -> R (IN REF. 2).

S -> T (IN REF. 2).
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Pred. No. 0.24;
6; Mismatches 92;
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EXTRACELLULAR (
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (PC
2 (POTENTIAL).
EXTRACELLULAR (
3 (POTENTIAL).
CYTOPLASMIC (PC
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                                                                                            Euteleostomi;
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InterPro; IPR000276; GPCH
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR.
InterPro; IPR000372; LRR.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 4.
Pfam; PF01462; LRRNT; 1.
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S36452; S
PIR; JN0898; J
HSSP; P23945;
                                                                     REPEAT
REPEAT
REPEAT
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REPEAT
                                                                                                                                                                              TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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PRINTS; PR01143; FSHRECEPTOR.
SMART; SM00013; LRRNT; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis."; Biochem. Biophys. Res. Commun. 196:1066-1072(1993).-!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                        Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF THIS RECEPTOR IS MEDIATED ADENYLATE CYCLASE.
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Repeat;
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012473;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ferric reductase transmembrane component 6 precursor
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C;

Wedler H., Wanbutt R.;

Wedler H., Wanbutt R.;

Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).

-I- COFACTOR: FAD (PROBABLE).

-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-I- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Ferric-chelate reductase 6).
FRE6 OR YLL0510 OR L0593.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEAST
                                                   EMBL; Z47973; CAA88006.1;
EMBL; Z73156; CAA97503.1;
SGD; S0003974; FRE6.
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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SIGNAL
                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
STRAIN-S288C
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                             NCBI_TaxID-4932;
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                                        Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
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EMBL; z49384; CAA89404.1;
SGD; S0003645; YJL109C.
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Rasmussen S.W.;
"A_37.5 kb region
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PROSITE; PS50077; HEAT_REPEAT; 1.
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or send an email to license@isb-sib.ch)
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                          hormone receptors and the nature of Structure 3:1341-1353(1995).
-!- FUNCTION: RECEPTOR FOR FOLLICLE
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95011044; PubMed=7926278; Gromoll J., Dankbar B., Gudermann T.; "Characterization of the 5' flanking regstimulating hormone receptor gene."; Mol. Cell. Endocrinol. 102:93-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93075197; PubMed-1359889;
Gromoll J., Gudermann T., Nieschlag E.;
"Molecular cloning of a truncated isoform
stimulating hormone receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tilly L.T., Aihara T., Nishimori K., Jai X.-C., Billig
Kowalski K.I., Perlas E.A., Hsueh A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chappel S.C.; "The cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Follicle stimulating hormone receptor precursor
                                                                                                                                                                                                                                                                                                                                     Hendrickson W.A., el Tayar N.;
                                                                                                                                                                                                                                                                                                                                                       Jiang X., Dreano M.,
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96363672; PubMed-8747461;
                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 188:1077-1083(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The cloning of the human follicle stimulating its expression in COS-7, CHO, and Y-1 cells."; Mol. Cell. Endocrinol. 89:141-151(1992).
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                                                                                                                                                                                                                                                                                                                        "Structural predictions
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                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                             ADENYLATE CYCLASE.
SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                           OF THIS RECEPTOR IS MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., Nakamura K., Takakura Y., Ibuki Y., Igar and sequencing of human FSH receptor cDNA."; Biophys. Res. Commun. 175:1125-1130(1991).
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Primates;
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the EMBL/GenBank/DDBJ
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Catarrhini; Hominidae
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G PROTEINS WHICH ACT
                                                                                                                                                                                                                                                                                                           hormone-receptor interactions.";
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.D., Kuzeja J.E
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GCRDb; GCR_0588; -.
GCRDb; GCR_0690; -.
MIN; 136435; -.
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InterPro: IPR001611; LRR.
InterPro: IPR000372; LRR_Nterm.
Pfam; PF000001; 7tm_1; 1.
Pfam; PF00560; LRR; 4.
Pfam; PF01662; LRRNT; 1.
Pfam; PF00173; GLYCHORMONER.
PRINTS; PR00173; FSHECEPTOR.
SMART; SM00013; LRRNT; 1.
                                                                                                                             CONFLICT
                                                                                                                                                                                CARBOHYD
CARBOHYD
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                                                                                                     CONFLICT
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REPEAT
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                                                                                                                                               CONFLICT
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                       CONFLICT
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 122
                  86
                                  79
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1XUN; 15-MAY-97.
INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                 HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG---
                HEIRIEKANNL-LYINPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNIN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M95489;
X68044;
S73199;
                                                          Similarity
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA52477.1;
AAB26480.1;
AAA52478.1;
CAA48179.1;
AAB32071.1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat;
                                                                                             GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

NISSING (IN SHORT ISOFORM).

MISSING (IN SHORT ISOFORM).

13 S -> R (IN REF. 4).

14 N -> T (IN REF. 1).

15 N -> T (IN REF. 1).

16 EL -> AV (IN REF. 1).

17 S -> P (IN REF. 1).

18 S -> P (IN REF. 1).

19 N -> T (IN REF. 1).
                                                                                            680
78294 MW;
                                                          4.2%;
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                                                   81;
                                                                                                                                                                                                                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                 Score 106; DB
Pred. No. 3.8;
81; Mismatches
                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
2 (POTENTIA
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                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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FOLLICLE STIMULATING HORMONE RECEPTOR
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                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                   148;
                                                                                            CRC64;
                                                                 Length
                                                 Indels
                                 -KILIDVSNNMR 121
                                                  198;
                                                 Gaps
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                                                             STRAIN-0157:H7 / KIMD 0509952;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-i- FUNCTION: Involved in the efflux of sugars. The physiologica may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the intracellular concentration of the may be the reduction of the may be the reduction of the intracellular concentration of the may be the reduction of the may be the
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_ECO57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugar efflux transporter.
SOTB OR Z2173 OR ECS2135.
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apodaca J., Anantharaman T
Welch R.A., Blattner F.R.;
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          sugars or sugar metabolites. Transports L-arabinose and to a lesser extent IPTG. Seems to contribute to the control of the arabinose regular /rm -right-regularity
  arabinose regulon (By similarity)
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SINILARITY: BELONGS TO THE MAJUK FACE.

THE DRUG RESISTANCE TRANSLOCASE FAMILY).
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                                                             IGYVG-TVPAFAALIWSIIIFRRWPVTLEEQ
                                                                                 LGYVALLISTFHVLIYG
                                                                                                    TAMMIIGLGMQVKVLALAPDATDVAMALFSGIFNIGIGAGALVGNQVSLHWS----
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BAB35558.1;
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wetween the Swiss Institute of Bioinformatics and the up the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usano had entities requires a lippon -
                                                                                                                                                                                                                              "Escherichia coli gene ydeA encodes a major facilitator pump which exports L-arabinose and isopropyl-beta-D-thiogalactopyranoside.";
J. Bacteriol. 181:5123-5125(1999).
-I-FUNCTION: Involved in the efflux of sugars. The physiological remay be the reduction of the intracellular concentration of toxi sugars or sugar metabolites. Transports L-arabinose and to a sugars or sugar metabolites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97251357; PubMed-9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Kasai H., Kashimoto K., Kimura S., Mori H., Mori T., Motomura Makino K., Miki T., Mishimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Washimoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Washimoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Washimoto Y., Horiuchi T., Baba Sampei Gorresponding to the 28.0-40.1 min region on the linkage map. DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                             Bost S., Silva F., Belin D.;
"Transcriptional activation of ydeA, which encodes a member of the major facilitator superfamily, interferes with arabinose accumulation and induction of the Escherichia coli arabinose PBAD promoter.";
J. Bacteriol. 181:2185-2191(1999).
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"Genetic and functional analysis of the multiple
resistance (mar) locus in Escherichia coli.";
J. Bacteriol. 175:1484-1492(1993).
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Sugar efflux transporter.
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port; Sugar transport;
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protein AQ_1349.
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Bacteria; Aquificales; A
NCBL_TaxID=63363;
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           061983;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Renal sodium-dependent phosphate transporte protein 1 (Sodium/phosphate cottransporter 1) (Renal sodium-phosphate
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aqu
  SLC17A1 OR
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Eukaryota; Metazoa; Chordata;
Mamumalia; Eutheria; Rodentia;
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MGI:103209; Slc17a1.
rPro; IPR003662; sub_transporter.
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                                                            KQLGLLSFFFAMVHVAYSLC - - LPMRRSE - - - -
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86; Conservative
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theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hughes M.R.;
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B0304.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000344; S Pfam; PF02117; Sra; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO C.ELEGANS B0304.6 AND B0304.7.
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Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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HSSP; P23945; 1XU
GCRDb; GCR_1561;
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01-FEB-1996 (Rel. 33, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin
                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                              This SWI
between
                                                                                                                                                                                                                                                                                             "Porcine follicle-stimulating hormone receptor.";
Submitted (SEP-1997) to the EMBL/GenBlank/DBJ databases.
-i- FUNCTION: RECEPTOR FOR FOLLICLE STRUILATING HORMONE. THE POF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Ovary;
MEDLINE=90011644; PubMed=7590277;
MEDLINE=96011644; PubMed=7590277;
Remy J.J., Lahbib-Mansais Y., Yerle M., Bozon V., Couture L
Pajot E., Grebert D., Salesse R.;
"The porcine follitropin receptor: cDNA cloning, functional
expression and chromosomal localization of the gene.";
Gene 163:257-261(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIG
                                                                        EMBL; L31966; AAA86933.1;
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SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                  ADENYLATE CYCLASE.
                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                     Y.F., Meyer K.B.,
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 IPR000276; GPCR_Rhodpsn.
IPR001611; LRR.
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                                                            AAC24981.1; -.
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PRINTS; PR01143; FSHRECEPTOR.
SMART; SM00013; LERNT; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled_receptor; Transmembrane; Glycoprotein; Signal;
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                                         THHEDALTKTNIIFVAIHREHYTSLWDLRHLLVG-----
                                                                                                                                       LPNG-INGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV
--HEIRIEKANNL-LYIDPDAFQNLPNLRYLLISNTGVKHLPAVHKIQSLQKVLLDIQDN
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                                                                                                                                                                                      91;
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                         Conservative
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N-N-LINKED (IN REF. 1).

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CYTOPLASMIC (F
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Pred. No. 6
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E9EBEDB29C79C450
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	520 MÖIDSPLSQLYVVSLLVLNVLAFVVIC 546	д В
	440SIVIIGKILFLPC 453	Oy '
519	460 LTAITLERWHTITHAMQLQCKVQLRHAASIMLVGWIFAFTVALFPIFGISSYMKVSICLP 519	ob 4
439	400 YVALLISTEHVLIYGWKRAFEEEYYRFYTPPNFV-LALVLP	Dy 4
459	409	9
399	352 EEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLG 399	Dy :
408	365 LRVLIWFISILAITGNIIVLVILITSQYKLTVPRFLMCNLAFAD	ob U
351	307LLSFFFAMYHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNE 351	Σy
364	305 TQARGQRVSLAEDGESSLAKEFDTMYSEFDYDLCNEVVDVICSPEPDTFNPCEDIMGHDI 364	9
306	268SLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG 306	Dy S
304	245 RAKSTYNLKKLPSLEKFYTLMEASLTYPSHCCAFANWRRQISDLHPICNKSILRQEVDVM 304	9
267	240 ARNOQSDEYKIPIEIVNKTL 267	Σ _Y
244	190FNGTQLDELNLSDNDNLEELPNDVFQGASGPVILDISRTRIHSLPSYGLENLKKL 244	9
239	180 ELARQUNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPY 239	Dy
189	155 INIHTVERNSFVGLSFESMILWLSKNGIREIHNCA 189	Db 1
179	120 MRINQYPESNAEYLASLFPDSLIVKGENVVSAWALQLGPKDASRQVYICSNNIQARQQVI 179	Ωy

Search completed: May 9, 2002, 03:23:06 Job time: 4216 sec

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_19:*

1: Sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1:
9: sp_phage:*
10: sp_plant:*
11: sp_virus:'
13: sp_verteb;
14: sp_unclas:
15: sp_vacterins:
16: sp_bacterins:
17: sp_archea:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 2000000000
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09120 sus scrofa
0924z2 mus musculu
092419 mus musculu
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092411 mus musculu
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099P41;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLEL. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-DUNNING; TISSUE-PROSTATE CANCER TUMOR;
Lu Y., Rinaldy A.R., Steiner M.S.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF335281; AAK00361.1; -.
SEQUENCE 488 AA; 54640 MW; 59FF07121919FDCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-DUNNING; TISSUE-PROSTATE CANCER TUMOR;
MEDIJINE-20424188; PubMed-10969787;
Steiner M.S., Zhang X., Wang Y., Lu Y.;
"Growth inhibition of prostate cancer by an adenovirus expressing novel tumor suppressor gene, pHyde.";
Cancer Res. 60:4419-4425(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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LVDSDGSLAE--VP-----KEAPK--VGILGSGDFARSLATRLVGSGFFVVVGSRNPKR 63
                                                                                                                                                              MMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKF 65
                                                                                                                                                                                                                                                                        258;
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                                                                                                                                                                                                                                                                                                            54.6%;
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Pred. No. 4.8e
88; Mismatches
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4.8e-101;
hes 106;
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Best Local S
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Q924Z1;
O1-DEC-2001 (TrEMBLrel. 19, Las
O1-DEC-2001 (TrEMBLrel. 19, Las
O1-DEC-2001 (TrEMBLrel. 19, Las
DUDULIN 2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
                                                                                                                                                                                                                                                         Kellermann O., Loric S.;

Molecular cloning and expression of mouse duc

Submitted (APR-2001) to the EMBL/GenBank/DDBJ

EMBL; AY029586; AAK50539.1;

SEQUENCE 514 AA; 57268 MW; 339886C288AECO
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Serru V., Lamblin D.,
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                           QYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELAR
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ENKFYKMPLSVVNTTLPCVAYVLLSLVYLPGVLAAALQLRRGTKYQRFPDWLDHWLQHRK
                  QSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRK
                                                                               QHRQSNAEYLASLFPACTVVKAFNVISAWALQAVPRDGNRQVLICGNDSKAKQRVMEMAR
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"Dudulin 2, a new tumor antigen es
Submitted (APR-2001) to the EMBL/C
EMBL; AK001691; BAA91839.1; -
EMBL; AK001691; BAAS1638.1; -
Interpro; IPR003006; Ig_MHC.
PROSITE; PS002300, IG_MHC; UNKNOWN,
SEQUENCE 488 AA; 54616 MW; BCC
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SUZUKİ

NASSIKAWA T., Ota T., Hayashi K., Sugiyama T., Otsuki S., Yoshikawa Y.,

NASSIKAWA T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,

MATERIA N., Yamamoto J., Wakan

NASAMURA Y., Nagahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCD-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ10829 FIS, CLONE NT2RP4001138 (DUDULIN 2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Local Similarity 53.1%;
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Pred. No. 7.8e-99;
1; Mismatches 121;
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Best Local S
Matches 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q923B6 PRELIMINARY; PRT; 470 AA.
Q923B6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO HYPOTHETICAL PROTEIN FLJ23153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                             CIDKTLTRIRQGWERNSKYTQSALNG
                                                        CISRKLKRIKKGWEK-SQFLEEGIGG
                                                                                                                                      RNATITQALTNKDSPFITSYAWINDSYLALGILGFFLFLLLGITSLPSVSNMVNWREFR
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                                                                                                      FIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVILGKIILFLP
                                                                                                                                                  FLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFS
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Pred. No. 6.7e-82;
9; Mismatches 141;
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Best Local Similarity
Matches 212; Conserv
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Q91ZE8;
Q91ZE8;
01-DEC-2001 (TFEMBLrel. 19, C
01-DEC-2001 (TFEMBLrel. 19, I
01-DEC-2001 (TFEMBLrel. 19, I
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Q91W31;
01-DEC-2001
01-DEC-2001
01-DEC-2001
  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN-SWISS; TISSUE-ADIPOSE TISSUE;
MEDLINE-21424005; pubMed=11443137;
Moldes M., Lasnier F., Gauthereau X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pred. No. 2.4e
90; Mismatches
Craniata; Vertebrata;
Sciurognathi; Muridae;
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Sciurognathi; Muridae;
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2.4e-81;
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; Murinae; Mus
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Serru V., Lamblin D., Manivet P.,
Kellermann O., Loric S.;
"Molecular cloning and expression
family.";
                                                                        SEQUENCE FROM N.A.

Nagasaka T., Boulday G., Coupel 9

Heslan J.-M., Soulillou J.-P., Cl

"Differential gene expression in
and LPS-mediated activation.";
                                    Submitted (NOV-2000) to the EMBL; AF319659; AAG33868.1;
                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIX TRANSMEMBRANE ENDOTHELIAL ANTIGEN OF PAEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; AY029778; AAK40270.1; -. SEQUENCE 474 AA; 53543 MW; 937EEA3393D139
  Transmembrane
SEQUENCE 338
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[1]
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Cetartiodactyla; Suina; Suidae;
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Loric S.;
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Q924Z2;
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                                                                                                                                                                                                                                                                             "Prostate and non-prostate of human STEAP.";
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Eukaryota; Metazoa;
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KKEPHWLDRWMVTRKQEGLLSEFEAVLHAVYSLSYPMRRSYRYKLLNWAYQQVQQNKEDA
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LCLPCLRKKILKIRCGWE
                                       REFHYIQSKLGIVSLLLGTVHALVFAWNKWVDVSQFVWYMPPTFMIAVFLPTLVLICKIA
                                                REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVILGKII
                                                                           HRYDLVNLAVKQVLANKEDAWVEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLTW
                                                                                                                                                          FPNWRLPVKVAAIISSLTFLYTLLREIIYPLVTSREQYFYKIPILVVNTTLPCVAYVLLS
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Rodentia;
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Pred. No. 1.2e-52;
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Pred. No. 2.9e-55;
4; Mismatches 78;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
KA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.:
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Matches 137
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Mus musculus (Mouse).
**Tervota; Metazoa; Chordata;
**horia; Rodentia;
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EMBL; AK010437; BAB26938.1; -.
MGD; MGI:1917608; Steap.
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55; Mismatches
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(STRAIN-C578L/6J; TISSUE-TESTIS;

(STRAIN-C578L/6J; TISSUE-TESTIS;

(X MEDLINE-21085660; PubMed-11217851;

(X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

(X Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

(X Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

(X Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

(X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

(X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

(X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

(X Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

(X Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

(X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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(X Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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MEDLINE-21371909; PubMed-11479226;
Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
Murine six-transmembrane epithelial antigen of the prostate, prostate stem cell antigen, and prostate-specific membrane antigen: prostate-specific cell-surface antigens highly expressed in prostate cancer of
                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Q9D5R1
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SEQUENCE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cancer Res. 61:5857-5860(20)
EMBL; AF297098; AAK83126.1;
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                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                              4921538B17RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic adenocarcinoma mouse prostate Cancer Res. 61:5857-5860(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFLPCISRKLKRIKKGWE
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                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                              (Mouse).
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Rodentia;
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Rodentia;
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5; Mismatches
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1.6e-52;
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Best Loc
Matches
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Best Local Similarity
Matches 123; Conserv
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KAWAKAMI T., Noguchi S., Itoh T., Shigeta K., Sei

Kawakami T., Mizuno T., Morinaga M., Tanigami A.

Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori N.

Obayashi M., Nishi T., Shibahara T., Tanaka T., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ da

EMBL; AKOZ6806; BAB15559.1;

TANACAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9H5RI;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CDNA: FLJ23153 FIS, CLONE LNG09441.
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                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000585; Hemopexin.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
SEQUENCE 283 AA; 31814 MW; DDD330D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AKO15015; BAB29672.1; -.

MGD; MGJ:1921301; 4921538817Rik.

SEQUENCE 132 AA; 14931 MW; B56F8732AEBEAFE3 CRC64;
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NCBI_TaxID=9606;
     130
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Local Similarity
hes 123; Conserv
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AEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIP
                                                                                  FPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNWRINQYPESN
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Pred. No. 1e-41;
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Pred. No. 3e-43;
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Tanigami A., Fujiwara T., Ono T.,
M., Ohmori Y., Ota T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
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Best Local Similarity
Matches 106; Conserv
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01-DEC-2001 (TIEMBLrel. 12, Last sequence up
WUGSC:H_RG087E15.1 PROTEIN (FRAGMENT).
WUGSC:H_RG087E15.1.
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SEQUENCE
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MEDLINE-99063792; PubMed-9847074;
Sulston J.E., Waterston R.;
"Toward a complete human genome sequence.
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL; AC005061; AAD43182.1;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Strong C., Layman D.,
"The sequence of Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1998)
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                                                                                                                                                                                                                                                                                                                              Waterston
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                                           257
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                                                                                                                                                                                      208 LFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
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                                                                                                                                           SLYYLAGILAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHYAYSLCLPMRR :|||| |::|| |::| ||| |||
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                                                                                                        SERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN 387
                                                                                                                               LFPQWHLPIKIAAVMASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLL
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264 AA;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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31203 MW;
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Primates;
                                                                                                                                                                                                                                22.8%;
                                                                                                                                                                                                                                                                                                                                                           , Graves T., Strowmatt C.; o sapiens BAC clone CTB-87E15."; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                    Score 577; DB
Pred. No. 9.8e
36; Mismatches
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Catarrhini;
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i; Hominidae;
                                                                                                                                                                                                                                DB 4;
1.8e-38;
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Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
                                                                                                                                                                                           MEDLINE-21396509; PubMed-11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium mellioti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007212; AAK64846.1; -.
EMBL; AE007212; AAK64846.1; -.
ENBL; AE007212; AAK64846.1; -.
ENBL; AE007212; AAK64846.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q930K7 PRELIMINARY; PRT; 198 AA.
Q930K7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN SMA0349.
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Nihomitya K., Iwayanagi T.,
Nihomitya K., Iwayanagi T.,
Nakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Nihomitya K., Iwayanagi T.,
Nihomitya K., Iway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-1021
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    Conservative
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                                     6.3%;
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Score 160; DB 16;
Pred. No. 5.3e-05;
0; Mismatches 83;
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Pred. No. 8e-25;
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                                                                      Length 198;
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The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign cryptorchidism, undescended, retractile, ascending or vanished cancer include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The
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                               sequence encodes a prostate specific protein, of Prostate 1, STMP1.
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The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 clone GTD3 cDNA. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing to the patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expresses STEAP, or inhibiting a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, or inhibiting growth or killing cells expressing STEAP, or inhibiting growth or killing cells expressing steap, that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                            New STEAP proteins, cancer -
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P-PSDB; AAE02781, AAE02841.
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entry)
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CDNA encoding ORF2 of Six-Transmembrane Protein 0f Prostate

RESULT
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ID AAS1
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AC AAS1
XX Humm
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                                                                                                                                                                                                                                                                                                                                                                           Sequence
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AAS15810 standard; ВP

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16-JAN-2002 (first entry)

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Six-Transmembrane

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testis-specific polypeptides and the nucleic acids encoding them. CC Also included are vectors and host cells expressing the proteins, a CC transgenic animal expressing the protein, antibodies against the CC proteins, probes for detecting the protein, antibodies against the CC proteins. Compounds that modulate the prostate specific or testis CC specific polypeptide are useful to diagnose, prevent or treat disorders compounds that modulate the prostate specific or testis CC of the testis or prostate particularly prostate cancer, benign CC prostatic hyperplasia, acute prostatitis, testicular cancer, cc cryptorchidism, undescended, retractile, ascending or vanished CC testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The prostate 1, STMP1, ORF3.
RESULT AASIULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÔ
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                                                                                      isolated polynucleotide (I) and essential essential (I) is useful as hybridisation probes.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as fet many contact the sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                  ry Match
t Local Similarity
ches 1218; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3900 BP; 1161 A;
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26-MAY-2000;
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03-AUG-2000;
21-SEP-2000;
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derived from mRNA of human breast, and then measuring the label

bound to each probe of the microarray. The probes are useful for

cerifying the expression of regions of genomic DNA predicted to

cencode proteins. They are useful for gene discovery, and for

cencode proteins. They are useful for gene discovery, and for

cetermining predisposition and/or prognosing breast disease. Gene

cexpression analysis is useful for assessing the toxicity of chemical

cagents on cells. The microarray of this invention presents a far greater

diversity of probes for measuring gene expression, with far less bias

than expressed sequence tag microarrays. The method is suitable for

crapid production of functional information from genomic sequence. The

present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this pattent did not form part of the

printed specification, but was obtained in electronic format directly

crapid production of functional information form part of the

printed specification, but was obtained in electronic format directly
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om human breast and
e probes with a co
                                                                                                                                                                                                                                                                                                 invention relates to a spatially-addressable set of single exoletic acid probes for measuring gene expression in a sample derination human breast and BT 474 cells. The method involves contacting probes with a collection of detectably labelled nucleic acids
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30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
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21-SEP-2000;
27-SEP-2000;
                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems. The probes are useful disease, hypertension, cardiac arrhythmias and e.g. cardiavascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                   Single
hearts
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                                                                                                                                                                                                                                                           Claim
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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congenital heart disease.
Note: The sequence data for this specification, but was obtained i

a for this patent did not obtained in electronic for

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21 - SEP - 2000;
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Local Similarity 99.3%;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers
                                                                                                                                                                                                                                                                                                             Sequence 1953
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533; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                              Conservative
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; leukaemia; lymphoma; myeloma; ss.
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Query Match Best Local S Matches 533

il Similarity 99.: 533; Conservative

28.1%; 99.3%;

Score 530.6; Pred. No. 6.5e 0; Mismatches

DB 22; 5.5e-147; 4;

Length

1953; 0;

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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPR at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                       analyzing
  Sequence
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                                                                                                                                                                                                                                                           invention relates to human single exon nucleic acid probes present sequence is one such probe. The SENPs are derived
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Search completed: May 9, 2002, 02:12:01 Job time: 13401 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-030-607-214
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US-09-323-873A-1
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APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Marthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
FILE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOR
FILE REFERENCE: 129.16USU2
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 05/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 521; Conserv
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US-08-940-035A-7
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US-08-854-050-68
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US-08-814-052-17
US-08-814-052-18
US-08-939-218A-1
PCT-US95-06815-1
US-08-706-037-26
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                                                                                                                                                                                                                                                                                                                      Mismatches
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le-148;
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Sequence 17, Appl
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Sequence 14, Appl
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Sequence 15, Appl
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Result

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Gaps

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Post-processing: Minimum Match 0%

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US-09-083-521-3
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                                                                Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 99,132
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROSTATI
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                                                              Local Similarity hes 477; Conserv
                                                                                                                                                                                                                     LENGTH: 1213 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: P
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STATE: CALIFORN:
COUNTRY: USA
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                                                             Score 476.4; DB 3;
Pred. No. 6.7e-135;
0; Mismatches 1;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 214, Application US/09030607
                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                      TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xú, Jiangchun APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUN NUMBER OF SEQUENCES: 224
                 MOLECULE TYPE:
                                                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tactttccatgttttaatttatggatggaaacgagcttttgaggaagagtactacagatt 1591
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                                                                                                                                                                                                                                                                                            US/09/030,607
                                                                                                                                                                                          210121.427C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   701 Fifth Avenue
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Query Match Best Local Similarity

22.5%;

Score Pred.

425.8; DB 4; No. 8.7e-120;

Length 444;

Matches

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: NAME/KEY: misc_feature
: LCCATION: (1)...(444)
: OTHER INFORMATION: n - A,T,C
US-09-439-313-214
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                  Matches
                                Query Match
Best Local Similarity
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 214
LENGTH: 444
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 214, Application US/09439313 Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                 APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
                                                                                                                                                                        ORGANISM: Homo sapien
                                                                                                                                                           FEATURE:
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Reed, Steven G.
Kalos, Michael
                                                                                                                                                                                                                                                                                                                                                                  Fanger, Gary
Retter, Mark
Solk, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon, Davin C.
Mitcham, Jennifer L.
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                  Conservative
                                22.5%;
98.6%;
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                  0;
                Score 425.8; DB 4;
Pred. No. 8.7e-120;
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                                               4.
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US-09-030-607-215/c
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US-09-030-607-215
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                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      CLASSIFICATION:
ATTORIEY/AGENT INFORMATION:
ATTORIEY MAKI, DAVID J.

NAME: MAKI, DAVID J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
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                           LENGTH: 366 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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6300 Columbia Center,
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; NAME/KEY: misc_feature
; LOCATION: (1)...(366)
; OTHER INFORMATION: n =
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Query Match
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                                                                                                                                                                  SEQ ID NO 215
                                                                                                                                                                        APPLICANT: SOIK, John
APPLICANT: DBY, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                  FEATURE:
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Retter, Mark
Solk, John
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Reed, Steven G.
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Mitcham, Jennifer L.
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Pred. No. le-100;
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOR
FITHLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOR
FILLE REFERENCE: 129.160502
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEG ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 322
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US-09-323-873A-9
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99.0%;
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Pred. No. 1.1e-84;
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GENERAL INFORMATION:
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 319; Conserv
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   TOPOLOGY: 111
MOLECULE TYPE:
9-030-607-212
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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APPLICANT: Dillon, Davin
TITLE OF INVENTION: COMPO
NUMBER OF SEQUENCES: 224
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CITY: Se
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COUNTRY:
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Pred. No. 1.2e-83;
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; OTHER INFORMATION: n = A,T,C
US-09-439-313-212
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APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan Louis
APPLICANT: Jiang Yuqui
APPLICANT: Read, Steven G.
APPLICANT: Kalos, Michael
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 212
LENGTH: 328
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
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Retter, Mark
Solk, John
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Pred. No. 1.2e
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; ORGANISM: Homo
US-09-323-873A-1
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APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129.16USU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/091,183 PRIOR FILING DATE: 1998-06-30 NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/087,520 PRIOR FILING DATE: 1998-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/323,873A CURRENT FILING DATE: 1999-06-01
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les 474; Conserv
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Pred. No. 2.7e-78;
0; Mismatches 306;
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Best Local Similarity
Matches 244; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                     1343 aaatattgaaaactcttggaatgaaggaagtttggagaattgaaatgtatatctcctt 1402
                                                                                                                                                         1283 accgatgagaaggtcagagagatatttgtttctcaacatggcttatcagcaggttcatgc 1342
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                  1403 tggcataatgagccttggcttactttccctcctggcagtcacttctatcccttcagtgag 1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: XU, Jiangchun APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 224
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
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TGGCATAATGAGCCTTGGCTTACTTTCCCTCCTGGCAGTCACTTCTATCCCTTCAGTGAG
                                                                  AAATATTGAAAACTCTTGGAATGAGGAAGAAGTTTGGAGAATTGAAATGTATATNTCCTT
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; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(250)
; OTHER INFORMATION: n = A
US-09-439-313-213
RESULT 13
US-09-33-873A-6
; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
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TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 213
LENGTH: 250
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Best Local Similarity 97.6
Matches 244; Conservative
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APPLICANT: Dillon, Davi
APPLICANT: Mitcham, Jen
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APPLICANT:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                          aaatattgaaaactcttggaatgaggaagtattggaggaattgaaatgtatatctcctt 1402
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Retter, Mark
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Mitcham, Jennifer L.
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APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.160SU2
CURRENT APPLICATION NUMBER: 1090/323,873A
CURRENT ETLING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
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; TYPE: DNA
; ORGANISM: HOMO S
US-09-323-873A-6
        TRESULT 14
US-09-439-313-342/c
; Sequence 342, Application
; Patent No. 6329505
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Matches 357
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LENGTH: 3627
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                                                                                                          atggagagaatttcactatattcag
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Pred. No. 2.9e-60;
0; Mismatches 208;
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Length 3627;

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Gaps

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994

352

412

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772

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652

INFORMATION:

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APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
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                                                                                                                                                                                                                                                                 Sequence 11, Application US/09323873A Patent No. 6329503
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Best Local,
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APPLICANT: Dillon, Davin C.
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Reed, Steven G.
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1; Mismatches 122;
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SEQ ID NO 11
LENGTH: 448
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Best Local Similarity 56.6%;
Matches 196; Conservative
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PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
              1673 tataagccgaaagctaaaacgaattaaaaaaggctgggaaaagagc 1718
                                                                                                                                         1493 tattcagtctacacttggatatgtcgctctgctcataagtactttccatgttttaattta 1552
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tgtagacaacaccttacaaggatccgccagggctgggaaaggaac
                                                          gttagggcttatcattccttgcactgtgctggtgatcaagtttgtcctaatcatgccatg
                                                                                                                        cggtgggaagagattcctcagcccttcaaatctcagatggtatcttcctgcagcctacgt
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Pred. No. 1.9e-22;
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Gaps 1432

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Search completed: May Job time: 13495 sec φ 2002, 02:06:15

329

269

209

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Result
No.
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Maximum DB seq length: 2000000000
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    411
377.8
366.6
343.2
326.6
321.8
310.2
275.4
277.8
272.8
272.8
272.8
272.8
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Query
Match
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BF883142 CV3-ET021
A2428664 1M0212F14
AK015015 Mus muscu
BM43143 B IDuo16F03
BI105662 602892429
BF784438 602110826
AK003108 Mus muscu
AA508880 ng86f03.s
BM491178 pgp2n.pk0
AI747886 uI03e11.y
AK010437 Mus muscu
BB603988 BB603988
AA957889 UI-R-E1-f
BI360480 387409 MA
BG565247 602582917
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ALIGNMENTS

FEATURES Source		TITLE JOURNAL COMMENT	RS ISM	RESULT 1 B1359597 LOCUS DEFINITION ACCESSION VERSION
BACKWARD: GTTTTCCCAGTCACGACG Plate: 132 row: H column: 3 Seq primer: ATTTAGGTGACACTATAG. Location/Qualifiers 1595 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC 2PIG" /tissue_type="mooiled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;	PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4356 Feax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR PRimers FORWARD: AGGAAACAGCTATGACCAT	Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) Contact: Smith TPL Contact: Smith TPL USDA. ARS, US Meat Animal Research Center	· 도면 및 및	595 bp mRNA linear EST 01-AUG-2001 384188 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI359597 BI359597.1 GI:15055625

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National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, N 20892-9643, USA
                                                                                                                                                                                                  BII33492 561 bp mRNA linear EST 02-JUL-
UI-M-BH3-brx-g-01-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone
UI-M-BH3-brx-g-01-0-UI 3', mRNA sequence.
                                    Contact: Chin, H
                                                Genome Res. 6 (9),
97044477
                                                                        discovery
                                                                                            Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 561)
Bonaldo, M. F., Lennon, G. and Soares, M. B.
                                                                                                                                            Mus musculus
                                                                                                                                                                               BI133492.1 GI:14583740
                                                                               Normalization and subtraction: two
                                                                                                                                                         house mouse
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92.6%;
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                                                                                  approaches
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FEATURES
                                                                                                                      oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the pineal glands tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
                                             POLYA=Yes
                                                                                  primer: M13 Forward
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301 443 9890
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                    /note="Vector: py7y31-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimattely derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research TAG_ELB-NIH_BMAP_M_S4

TAG_TISSUE-pineal-glands

TAG_EC-CAGAC 129 g 163 t
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/clone_lib="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B_(Life_Technologies)"
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Qy В δÃ 밁 Qγ

501

672 442

382

Matches 490; Query Match Best Local :

Local

Similarity

23.8%;

Score 451; DB Pred. No. 5.5e 0; Mismatches

DB 10; 5.5e-104; 1es 65;

Length 561; Indels

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Conservative

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493 gtagaaatcctaagtttgcttctgaattttttcctcatgtggtagatgtcactcatcatg 552

aagatgeteteacaaaaacaaatataatatttgttgetatacacagagaacattatacet 612

AAGATGCTTTAACAAAAACAAATATAATATTCGTGGCTATCCATAGAGAACATTACACCT

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                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0211-
071200-529-b10&t3=2000-12-07&t4=1)
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                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                       sequence tags
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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(bases 1 to 483)

(bases 1 to 483)

as Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
as Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Costa,F.F.,
                                                                                                            primer: puc 18 forward
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                                                                quality sequence start: 26 quality sequence stop: 483. Location/Qualifiers
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/clone_lib="ET0211"
/dev_stage="Adult"
                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                  plasmid inserts
Unpublished (2000)
                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 712)
          University of Utah Genome University of Utah
                                                                                                                                                                                                                                                 1M0212F14F Mouse 10kb plasmid UUGC1MC1one UUGC1M0212F14 F, DNA sequence.
                                       Contact: Robert B.
                                                                            Mouse whole genome
                                                                                                                                                                                  Mus musculus
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                                     tgggtaaaatcctgattgatgtgagcaataacatgaggataaaccagtacccagaatcca 699
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Class: plasmid ends
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nilarity 87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0212F14"
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/strain="C57BL/6J"
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                                                                                                                                Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yamanaka, I.,
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Mus musculus adult male testis CDN/
library, clone:4921538B17:homolog t
MAMMA1000859, full insert sequence
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
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                                                          Direct Submission
                                                                                 Hayashizaki,Y
                                                                                                                 Yasunishi,A.,
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5 (bases 1 to 2473)
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                Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohar Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/clone_llb="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
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                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                          /lab_host="XL1-BlueMRF'strain"
/note="Organ: Intestine/duodenum;
Site_1: EcoRI; Site_2: xho I"
109 c 108 g 189 t
                                                                                                                                                                                                                                                                                                       /clone_lib="Bos taurus Duodenum #1 library"
/tissue_type="Smooth muscle"
/ceil_type="Simple columnar epithelial"
/dev_stage="Young adult"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus'
/db_xref="taxon:9913"
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Pred. No. 2.6e-82;
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| lenum #1 library Bos taurus cDNA, mRNA
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                                                                                                                                                                                                                                                                            Vector: Uni-2ZAPXR;
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Best Local (
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    440;
                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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602892429F1 NCI_CGAP_Lu29 Mus
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plate: LLAM11103 row: j column:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BI105662.1 GI:14556555
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                 Similarity
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                                                                                                                                                                                                                                                                                         quality sequence stop: 674.
Location/Qualifiers
1.677
    Conservative
                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C2ECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:5037414"
/clone_lib="NCI_CGAP_Lu29"
                                                                                        /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Site_2: NotI; Cloned unidirectionally. Primer: (Library constructed by Life Technologies. Invest: providing samples: Gilbert Smith, NIH" 172 c 160 g 168 t
                                                                                                                                                                     /tissue_type="spontaneous
Stem cell origin."
/lab_host="DH10B"
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                 18.1%;
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Rodentia;
Score 343.2; DB 10
Pred. No. 1.8e-76;
0; Mismatches 68;
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BF784438.1
                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF784438 948 bj 602110826F1 NCI_CGAP_Kid14 Mus 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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National Institutes of Health, P
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 948)
                                                                                                                                                    quality sequence
/Strain="TVB/N"
/strain="TVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4238935"
/clone_lib="NCI_CGAP_Kid14"
/clone_lib="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6;
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                                                                                                        organism="Mus musculus"
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IMAGE:4238935
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                                                                                  Meth. En 99279253
                                                                                              Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                   HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult

Mus musculus (strain:C57BL/6J) adult
                                                                                                                                                                                                                                                                                                                  AK003108 1287 bp mRNA Mus musculus adult male heart cDNA, RIKEN library, clone:1010001D01:homolog to CDNA
              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
    Normalization
                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                           clone:1010001D01.
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Technologies. Note: this is a NCI_CGAP Library. | "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiranoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yashida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Labburatory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                  cleaved with XhoI and SstI. Cloning sites,
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The RIKEN Genome Exploration Research Group
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                              /tissue_type="heart"
/clone_lib="RIKEN full-length enriched
/dev_stage="adult"
1. .1287
                                                                                                                                                                                                                                                                  /strain="C57BL,
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/strain="C57BL/6J"
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                                                                 tttttcttcgctatggtccatgttgcctacagcctctgcttaccgatgagaaggtcaga
                                                                                                                                                                                                                                 aattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccct 1120
CCGCTACGACCTGGTCAATCTGGCTGTGAAGCAGGTCCTGGCCAACAAGAGCCGCCTCTG
                gagatttccaccttggttggaaacctggttacagtgtagaaaacagcttggattactaag
                                                                                                                                                                          agtatacctcgcaggtcttctggcagctgcttatcaactttattacggcaccaagtatag
                                                                                                                                                                                                                                                                                   ttcctttgtcagagatgtgattcatccatatgctagaaaccaacagagtgacttttacaa 1060
                                                                                                                                                                                                                                                                                                                                           CCTGGACATGGGATCCCTGGCCTCAGCGAGGGAGGTAGAAGCCATACCCCTGCGCCTCCT
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                                                                                                       GCGCTTCCCAGACTGGCTGGACCACTGGCTGCAGCATCGCAAGCAGATCGGGCTGCTCAG
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                                                     AGTGTACCTGCCCGGTGTGCTGCCAG-TGCGCTTCAGCTGCGGAGGGGGACCAAGTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTGAGTACCTGGCCTCACTCTTTCCTGCGTGCACTGTGGTGAAGGCCCTTCAACGTCAT
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                                                        Local Similarity 99.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing distribution: NCI-CGAP clone distribution infi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGTTGTCGCTGGCTGGCTGTCACCTCGCTCCGTCCATTGCTAATTCCCTCAACTGGAA 1197
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1000 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 249.
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ng86f03.sl NCI_CGAP_Pr6
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National Cancer Institute, Cancer Genome Anatomy
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 322)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                         84
                                                                                                                                                                                                     /note="Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (low-grade), cDNA made b oligo-dT prining. Non-directionally cloned. Size-selected on agarose gel, average insert size Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                         /tissue_type="prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pr6"
                                                                                                                                                                                                                                                                                                                                                                     /clone-"IMAGE:941693"
                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                              16.4%;
99.0%;
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                                                                                                                  Score 310.2;
Pred. No. 3.6e
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cDNA clone IM
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pgp2n.pk005.j8 Normalized Chicken Pituitary/Hypothalamus/Pineal
Library (pgp2n) Gallus gallus cDNA clone pgp2n.pk005.j8 5′ simi
to gb|AAK50539.1 (AY029586) dudulin 2 [Mus musculus], mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                           Townsend Hall, Newark, DE 19717,
                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porter,T.E. and Cogburn,L.A.
ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus
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                                                                                                                                                           150
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                  cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                        /lab_host="E. coli EMDH10B"
/note="Vector: pcMvSPORT6; Library made from equivalent
/notes of total RNA isolated from each tissue at different
pools of total RNA isolated from 5'-end"
ages. Single pass sequencing from 5'-end"
153 c 144 g 126 t
                                                                                                                                                                                                                                   /sex="Male and Female"
/tissue_type="pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7)
                                                                                                                                                                                                                                                                         /clone="pgp2n.pk005.j8"
/clone_lib="Normalized Chicken
Pituitary/Hypothalamus/Pineal Library (pgp2n)"
                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/strain="Commercial broile
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:931"
/clone="nomposition:"/db.
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                          14.6%;
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                                                                              0;
                                                                                         Score 275.4;
Pred. No. 3.3
                                                                              Mismatches
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                                                                                                      DB 10;
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                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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GAGAACACTACACGTCTTTGTGGGACCTCAAGCATTTACTCGTCGGTAAAAATTCTGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ul03e11.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2055004 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pe., B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ri, E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-NCI Mouse EST Project 1999
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                               primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 498
/dev_stage="adult"
/lab_host="DH108"
/lab_host="DH108"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                      /sex="female"
                                                                                                                                                                                  /clone_lib="Sugano mouse
                                                                                                                                                                                                          /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2065004"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Munatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                               Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1211 bp mRNA linear HTC 19-J.
Mus musculus ES cells cDNA, RIKEN full-length enriched libra-
clone:2410007B19:six transmembrane epithelial antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (strain:C57BL/6J) ES cells cDNA to clone_lib:RIKEN full-length enriched mouse cDNA
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HTC; CAP trapper.
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1 135 c 126 g 134 t
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                                     for rapid discovery of new genes
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library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           raysucal and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
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/db_xref="G1:12845881"
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/translation="MEISDDVTNPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLS
/translation="MEISDDVTNPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLS
HLQHAVHVDAFDCPSELOHTQEFFPNWRLPVKVAAIISSLTFLYTLLREIIYPLVTSR
EQYFYKIPILVINKVLPMVAITLLALVYLPGELAAVVQLRNGTKYKKFPPWLDRWMLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., I
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsu
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
N.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Suc,Y. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                      Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science Division of Experimental Animal Research in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONdo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Arakawa, T., Carninci, P., Fukuda, S.,
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                    /db_xref="taxon:10090"
/clone="D930007L06"
                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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n Riken contributed t
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AA957889.1 GI:4277779
1 (bases 1 to
Bonaldo, M.F., I
                                                                                     Norway rat.
Rattus norvegicus
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                                   Rattus
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Mammalia; Eutheria;
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AAGACGCTTTAACGAAGACAAATATAATATTCGTGGCTATCCATAGAGAACATTACACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On May 7, 1998 this sequence version replaced
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-wester pm713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-E1 library is a subtracted library derived from the UI-R-E0 library. The UI-R-E0 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-E1) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-E0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-E0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-EI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-E1-Ev-a-01-0-UI"
/clone_lib="UI-R-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B_(Life_Technologies)"
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87.2%;
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